

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:31:45 ; Search time 14.38 seconds  
(without alignments)  
783.994 Million cell updates/sec

Title: US-09-016-869B-35

Perfect score: 760  
Sequence: 1 MEPSADWLATAAARGVEEV.....TRGSNHARIDAEGPSDIPD 148

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	99.1	156	2 JE0141	cyclin dependent k
2	529	69.6	130	2 I78845	p15INK4b - mouse
3	522	68.7	138	2 B55479	CDK4 inhibitor p14
4	461.5	60.7	167	2 I58352	p16INK4a - mouse
5	258	33.9	164	2 A57378	cyclin-dependent k
6	249	32.8	166	2 A57379	CDK4/CDK6 inhibito
7	244	32.1	166	2 B57378	cyclin-dependent k
8	231.5	30.5	168	2 B57379	CDK4/CDK6 inhibito
9	228.5	30.1	168	2 A55479	CDK6 inhibitor p18
10	209	27.5	41	2 I52720	gene p15INK4B prot
11	158	20.8	3924	2 S37431	ankyrin 2, neurona
12	137.5	18.1	1848	2 S37771	ankyrin, erythrocy
13	137.5	18.1	1862	2 I49502	ankyrin - mouse
14	133.5	17.6	1836	2 B35049	ankyrin 1, erythro
15	133.5	17.6	1880	2 A35049	ankyrin 1, erythro
16	133.5	17.6	1881	1 SJHUK	ankyrin 1, erythro
17	131	17.2	857	2 S62694	potassium channel
18	130.5	17.2	1423	1 I37275	death-associated p
19	130	17.1	838	2 S23606	potassium channel
20	130	17.1	1765	2 T42714	ankyrin 3, splice
21	130	17.1	1940	2 T42715	ankyrin 3, splice
22	130	17.1	1943	2 T42713	ankyrin 3, splice
23	130	17.1	1961	2 T42716	ankyrin 3, splice
24	128	16.8	4377	2 A55575	ankyrin 3, long sp
25	127.5	16.8	1786	2 A57282	ankyrin-related pr
26	127.5	16.8	1815	2 T15346	elegans ankyrin-re
27	127.5	16.8	1867	2 T15344	ankyrin-related un
28	127.5	16.8	2039	2 T15347	ankyrin-related un
29	126	16.6	247	2 D84448	probable ankyrin [

30	125	16.4	1964	2 T09059	notch4 - mouse
31	124.5	16.4	209	2 T15888	hypothetical prote
32	121	15.9	237	2 T50984	related to 26s pro
33	121	15.9	888	2 D84650	probable potassium
34	120	15.8	476	2 T23213	hypothetical prote
35	118.5	15.6	347	2 C40858	GA-binding protein
36	118.5	15.6	382	2 B40858	GA-binding protein
37	117.5	15.5	347	2 C48146	nuclear respirator
38	117.5	15.5	348	2 I38744	nuclear respirator
39	117.5	15.5	360	2 I38743	nuclear respirator
40	117.5	15.5	395	2 I38741	nuclear respirator
41	117	15.4	1435	2 T32930	hypothetical prote
42	116	15.3	1549	2 T13940	ankyrin - fruit fl
43	115.5	15.2	1058	2 D82654	potassium channel
44	114	15.0	828	2 T52046	transmembrane prot
45	114	15.0	2437	2 S42612	

#### ALIGNMENTS

RESULT 1

JE0141

cyclin dependent kinase inhibitor - human

N:Alternate names: CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase inhibitor

C:Species: Homo sapiens (man)

C>Date: 02-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 19-May-2000

C:Accession: JE0141; I59268; S39359; I59585; JC5679

R:Huang, C.G.; Deng, W.; Fu, J.L.

Chin, J. Biotechnol. 13, 105-107, 1997

A:Title: Molecular cloning and sequencing of p16 ink4 cDNA from hela cell.

A:Reference number: JE0141

A:Accession: JE0141

A:Molecule type: mRNA

A:Residues: 1-156 <HUA>

A:Experimental source: Hella cell

R:Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.; Hussain, S.P.; Bennett,

Proc. Natl. Acad. Sci. U.S.A. 91, 11045-11049, 1994

A:Title: Mutations and altered expression of p16INK4 in human cancer.

A:Reference number: I59268; MUID:95062202

A:Accession: I59268

A>Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-152 <OKA>

A:Cross-references: GB:L27211; NID:g558656; PIDN:AAA92554.1; PID:g558657

A:Note: the sequence is revised in GenBank entry HUMINK4x, release 113.0, PIDN:AAA925

R:Serrano, M.; Hannon, G.J.; Beach, D.

Nature 366, 704-707, 1993

A:Title: A new regulatory motif in cell-cycle control causing specific inhibition of

A:Reference number: S39359; MUID:94081956

A:Accession: S39359

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 9-34,'V',36-156 <SER>

A:Note: this sequence is corrected in reference I59268

R:Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavitigian, S.V.;

Science 264, 436-440, 1994

A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.

A:Reference number: I59585; MUID:94204645

A:Accession: I59585

A>Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 51-152 <KAM>

A:Cross-references: GB:S69804; NID:g546272; PIDN:AAI4048.1; PID:g4261748

C:Comment: This protein inhibits the activity of cyclin D1/CDK4 and cyclin D1/CDK6 k1

C:Genetics:

A:Gene: GDB:CDKN2A; CDK4I; MLM; PI6; INK4; MTS1; CMM2; CDKN2

A:Cross-references: GDB:335362; OMIM:600160

A:Map position: 9p21-9p21

C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol

C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match 99.1%; Score 753; DB 2; Length 156;  
Best Local Similarity 99.3%; Pred. No. 1.5e-64;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEVRALLAEVALPNAPNSYGRRPQVMMGSGARVAEILLHGA 60  
DB 9 MEPSADWLATAAARGVEVRALLAEVALPNAPNSYGRRPQVMMGSGARVAEILLHGA 68

QY 61 EPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120  
DB 69 EPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 128

QY 121 YLRAAAGGTRGSNHRIDAAEGPSDIPD 148  
DB 129 YLRAAAGGTRGSNHRIDAAEGPSDIPD 156

RESULT 2  
I78845  
p15INK4b - mouse  
C:Species: Mus sp. (mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 19-May-2000  
C:Accession: I78845  
R:Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.; W  
Oncogene 11, 635-645, 1995  
A:Title: Cloning and characterization of murine p16INK4a and p15INK4b genes.  
A:Reference number: I58352; MUID:95380169  
A:Accession: I78845  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-130 <RES>  
A:Cross-references: GB:S79252; NID:g1087092; PID:g1087093  
C:Genetics:  
A:Gene: p15INK4b  
C:Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homology

Query Match 69.6%; Score 529; DB 2; Length 130;  
Best Local Similarity 88.3%; Pred. No. 2.5e-43;  
Matches 106; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 8 LATAAARGVEVRALLAEVALPNAPNSYGRRPQVMMGSGARVAEILLHGAEPNCADP 67  
DB 10 LATAAARGVEVRALLAEVALPNAPNSYGRRPQVMMGSGARVAEILLHGAEPNCADP 69

QY 68 ATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVARVYLR 127  
DB 70 ATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVARVYLR 129

RESULT 3  
B55479  
CDK4 inhibitor p14(INK4B/MTS2) - human  
N:Alternate names: CDK6-associated protein p15(INK4B); cyclin-dependent kinase inhibitor  
C:Species: Homo sapiens (man)  
C:Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 21-Jul-2000  
C:Accession: B55479; S47593; I81183; I52713  
R:Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.;  
Genes Dev. 8, 2939-2952, 1994  
A:Title: Growth suppression by p18, a p16(INK4/MTS1)- and p14(INK4B/MTS2)-related CDK6  
A:Reference number: A55479; MUID:95095079  
A:Accession: B55479  
A:Molecule type: mRNA  
A:Residues: 1-138 <GUA>  
A:Cross-references: GB:U17075; NID:g639715; PIDN:AAC50075.1; PID:g639716  
A:Experimental source: HeLa cells  
R:Hannon, G.J.; Beach, D.  
Nature 371, 257-261, 1994  
A:Title: p15(INK4B) is a potential effector of TGF-beta-induced cell cycle arrest.  
A:Reference number: S47593; MUID:94359613  
A:Accession: S47593  
A:Molecule type: mRNA  
A:Residues: 1-19, 'TP', 22, 24-31, 'HSW', 35-138 <HAN>

A:Cross-references: GB:I36844; NID:g556197; PIDN:AAA50282.1; PID:g556198  
A:Experimental source: HaCat cells  
R:kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.;  
Science 264, 436-440, 1994  
A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.  
A:Reference number: I59585; MUID:94204645  
A:Accession: I81183  
A:Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 53-138 <KAN>  
A:Cross-references: GB:S69805; NID:g546273; PIDN:AAD14049.1; PID:g4261749  
R:Jen, J.; Harper, J.W.; Bigner, S.H.; Bigner, D.D.; Papadopoulos, N.; Markowitz, S.;  
Cancer Res. 54, 6353-6358, 1994  
A:Title: Deletion of p16 and p15 genes in brain tumors.  
A:Reference number: I52713; MUID:95079408  
A:Accession: I52713  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-52 <RES>  
A:Cross-references: GB:S75756; NID:g861470; PIDN:AAD14186.1; PID:g4261886  
C:Genetics:  
A:Gene: GDB:CDKN2B; MTS2  
A:Cross-references: GDB:579577; OMIM:600431  
A:Map position: 9p21-9p21  
C:Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homol  
C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match 68.7%; Score 522; DB 2; Length 138;  
Best Local Similarity 85.5%; Pred. No. 1.2e-42;  
Matches 106; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 4 SADWLATAAARGVEVRALLAEVALPNAPNSYGRRPQVMMGSGARVAEILLHGAEPN 63  
DB 14 SDEGLASAAAAGLVKVKVQLLEAGADPNVGRFRGRRATQVMMGSAKVAEILLHGAEPN 73

QY 64 CADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVARVYLR 123  
DB 74 CADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVARVYLR 133

QY 124 AAAAG 127  
DB 134 TATG 137

RESULT 4  
I58352  
p16INK4a - mouse  
C:Species: Mus sp. (mouse)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 24-Nov-1999  
C:Accession: I58352  
R:Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.  
Oncogene 11, 635-645, 1995  
A:Title: Cloning and characterization of murine p16INK4a and p15INK4b genes.  
A:Reference number: I58352; MUID:95380169  
A:Accession: I58352  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-167 <RES>  
A:Cross-references: GB:S79251; NID:g1087090; PID:g1087091  
C:Genetics:  
A:Gene: p16INK4a  
C:Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homol

Query Match 60.7%; Score 461.5; DB 2; Length 167;  
Best Local Similarity 63.2%; Pred. No. 8.5e-37;  
Matches 98; Conservative 16; Mismatches 32; Indels 9; Gaps 3;

QY 1 MEPSADWLATAAARGVEVRALLAEVALPNAPNSYGRRPQVMMGSGARVAEILLHGA 60  
DB 1 MESAADRLA-RAAQGRVHDVRLLEAGVSPNAPNSGRTPTIQVMMGNVHVVAALLNLYGA 59

DB 3 P M G N E L A A A A R G D J E O L T S L Q N N V N V N A Q N S F G S T A L Q V M K L G N P E I A R R L L L R G A N 62

QY 62 P N C A D P A T L T R P Y H D A A R G E F D T L V L H R A G A R L D V R D A G R L P V D I A E E L G H R D V A R Y 121

Db	63	PNLKD-GTGFVAVHDAARAGFLDTVQALFEQADVNIEDNEGNLPLHLAAKEGHLPVVEF	121
QY	122	LRAAAGGTRGSNHARIDAA	140
Db	122	LMKHTACNVGHRNHKGDTA	140
RESULT	9		
A55479			
CDK6			
N:Alternate names:		cyclin-dependent kinase inhibitor 2C; D-type cyclin-dependent kinase	
C:Species:		Homo sapiens (man)	
C:Date:		23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 20-Sep-1999	
C:Accession:		A55479	
R:Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.;			
Genes Dev.		8, 2939-2952, 1994	
A:title:		Growth suppression by p18, a p16(INK4/MTS1)- and p14(INK4B/MTS2)-related CDK6	
A:Reference number:		A55479; MUID:95095079	
A:Accession:		A55479	
A:Molecule type:		mRNA	
A:Residues:		1-168 <GUA>	
A:Cross-references:		GB:U10704; NID:g639713; PIDN:AA050074.1; PID:g639714	
C:Genetics:			
A:Gene:		GDB:CDKN2C	
A:Cross-references:		GDB:594931	
A:Map position:		lp32-lp32	
C:Superfamily:		unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology	
C:Keywords:		cell cycle control; protein kinase inhibitor; tumor suppressor	
Query Match		30.1%; Score 228.5; DB 2; Length 168;	
Best Local Similarity		40.3%; Pred. No. 1.2e-14;	
Matches		56; Conservative 22; Mismatches 60; Indels 1; Gaps 1;	
QY	2	EPSADWLATAAARGVEEVRALLEVALPNAPNSYGRPIQVMMGSAKVAVELLHGAE	61
Db	3	EPWGNELASAAAGDLBOLTSLQNNVNVNAQNGFGRTALQVWKLGPNPIARRLLRGAN	62
QY	62	PNCADPATLTPVHDAAREGFLDTLVLRHAGARLDVDAWGLPVDLAEELGHRDVARY	121
Db	63	PDLDK-RTGFAVHDAARAGFLDTLQTLLEFFQADVNIEDNEGNLPLHLAAKEGHLRVVEF	121
QY	122	LRAAAGGTRGSNHARIDAA	140
Db	122	LVKHTASNVGHRNHKGDTA	140
RESULT	10		
152720			
gene		p15INK4B protein - rat (fragment)	
C:Species:		Rattus sp. (rat)	
C:Date:		26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-May-2000	
C:Accession:		152720	
R:Knapek, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L.			
Cancer Res.		55, 1607-1612, 1995	
A:title:		Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in kidney epithel	
A:Reference number:		152720; MUID:95228036	
A:Accession:		152720	
A>Status:		preliminary; translated from GB/EMBL/DDBJ	
A:Molecule type:		DNA	
A:Residues:		1-41 <RES>	
A:Cross-references:		GB:S77734; NID:g998711	
C:Genetics:			
A:Gene:		p15INK4B	
C:Superfamily:		unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology	
Query Match		27.5%; Score 209; DB 2; Length 41;	
Best Local Similarity		97.6%; Pred. No. 1.7e-13;	
Matches		40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	44	MMGSAKVAVELLHGAEPNCADPATLTPRVHDAAREGFLD	84

Query Match 18.1%; Score 137.5; DB 2; Length 1848;  
Best Local Similarity 34.7%; Pred. No. 8e-05;  
Matches 51; Conservative 17; Mismatches 68; Indels 11; Gaps 6

QY	8	LATAARGVEEV	RALL	EAVAL	PNAPNSY	GRPTIQV	MMG	SARVAE	LLHLHG	AEPCAD	66
DB	503	LHTAAREGH	VDITAL	LEKEAS	QCMTK	GKGTPLH	VAAKYG	KVRLAE	LLLEH	DHPNAAG	562
QY	67	PATLTPV	HDAAREG	FLDTL	VVLH	RAGARLD	VDYDAW	GRLP	VDLAEEL	GHVDVARYL	122
DB	563	KNGLT	PLHVAVH	NNLDI	VKLLP	PGRS	--PHS	PAWNGYT	PLHTAAK	ONIEVARS	619

C:Date: 27-Jul-1990 #sequence\_revision 01-Oct-1992 #text\_change 04-Sep-1998  
C:Accession: A35049  
R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.  
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990  
A:Title: cDNA sequence for human erythrocyte ankyrin.  
A:Reference number: A35049; MUID:90175370  
A:Accession: A35049  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1880 <LAM>  
A:Cross-references: GB:M28880  
C:Genetics:  
A:Gene: GDB:ANK1; ANK  
A:Cross-references: GDB:118737; OMIM:182900  
A:Map position: 8p11.2-8p11.2  
C:Superfamily: ankyrin; ankyrin repeat homology  
C:Keywords: alternative splicing; cytoskeleton  
F:2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>  
F:2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>  
F:44-76/Domain: ankyrin repeat homology <AN01>  
F:77-109/Domain: ankyrin repeat homology <AN02>  
F:110-142/Domain: ankyrin repeat homology <AN03>  
F:143-171/Domain: ankyrin repeat homology <AN04>  
F:172-204/Domain: ankyrin repeat homology <AN05>  
F:205-237/Domain: ankyrin repeat homology <AN06>  
F:238-270/Domain: ankyrin repeat homology <AN07>  
F:271-303/Domain: ankyrin repeat homology <AN08>  
F:304-336/Domain: ankyrin repeat homology <AN09>  
F:337-369/Domain: ankyrin repeat homology <AN10>  
F:370-402/Domain: ankyrin repeat homology <AN11>  
F:403-435/Domain: ankyrin repeat homology <AN12>  
F:436-468/Domain: ankyrin repeat homology <AN13>  
F:469-501/Domain: ankyrin repeat homology <AN14>  
F:502-534/Domain: ankyrin repeat homology <AN15>  
F:535-567/Domain: ankyrin repeat homology <AN16>  
F:568-600/Domain: ankyrin repeat homology <AN17>  
F:601-633/Domain: ankyrin repeat homology <AN18>  
F:634-666/Domain: ankyrin repeat homology <AN19>  
F:667-699/Domain: ankyrin repeat homology <AN20>  
F:700-732/Domain: ankyrin repeat homology <AN21>  
F:733-765/Domain: ankyrin repeat homology <AN22>  
F:766-798/Domain: ankyrin repeat homology <AN23>

RESULT 14  
B35049  
ankyrin 1, erythrocyte splice form 3 - human  
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N:Contains: ankyrin 2.2, erythrocyte  
C:Species: Homo sapiens (man)  
C:Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 10-Jul-1998  
C:Accession: B35049  
R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K  
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990  
A:Title: cDNA sequence for human erythrocyte ankyrin.  
A:Reference number: A35049; MUID:90175370  
A:Accession: B35049  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1856 <LAM>  
C:Genetics:  
A:Gene: GDB:ANK1; ANK  
A:Cross-references: GDB:118737; OMIM:182900  
A:Map position: 8p11.2-8p11.2  
C:Superfamily: ankyrin; ankyrin repeat homology  
C:Keywords: alternative splicing  
F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>  
F:2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>  
F:44-76/Domain: ankyrin repeat homology <AN01>  
F:77-109/Domain: ankyrin repeat homology <AN02>  
F:110-142/Domain: ankyrin repeat homology <AN03>  
F:143-171/Domain: ankyrin repeat homology <AN04>  
F:172-204/Domain: ankyrin repeat homology <AN05>  
F:205-237/Domain: ankyrin repeat homology <AN06>  
F:238-270/Domain: ankyrin repeat homology <AN07>  
F:271-303/Domain: ankyrin repeat homology <AN08>  
F:304-336/Domain: ankyrin repeat homology <AN09>  
F:337-369/Domain: ankyrin repeat homology <AN10>  
F:370-402/Domain: ankyrin repeat homology <AN11>  
F:403-435/Domain: ankyrin repeat homology <AN12>  
F:436-468/Domain: ankyrin repeat homology <AN13>  
F:469-501/Domain: ankyrin repeat homology <AN14>  
F:502-534/Domain: ankyrin repeat homology <AN15>  
F:535-567/Domain: ankyrin repeat homology <AN16>  
F:568-600/Domain: ankyrin repeat homology <AN17>  
F:601-633/Domain: ankyrin repeat homology <AN18>  
F:634-666/Domain: ankyrin repeat homology <AN19>  
F:667-699/Domain: ankyrin repeat homology <AN20>  
F:700-732/Domain: ankyrin repeat homology <AN21>  
F:733-765/Domain: ankyrin repeat homology <AN22>  
F:766-798/Domain: ankyrin repeat homology <AN23>

Query Match 17.6%; Score 133.5; DB 2; Length 1880;  
Best Local Similarity 35.4%; Pred. No. 0.0002;  
Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;  
QY 8 LATAAARGVEVRALLEAVLPNAPNSYGRRTIQV-MMGSAARVAELLLHGAEPNCAD 66  
DB 507 LHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAAYKGVKRVVAELLLERDAHPNAA 566  
QY 67 PATLTRPVHDAAREGFLDTL-VVLRAGARLDVRDAW-GRLPVDLAELGHRDVARYL-- 122  
DB 567 KNGLT-PLHVAVHHNNLDIVKLLPRGGS--PHSPAANGYTPLHIAAKQNOVEVARSLIQ 623  
QY 123 ---RAAGGTRGSNHARIDAAGPSDI 146  
DB 624 YGGSANAESVQGVTPHLHAAQEGHAEM 650

Query Match 17.6%; Score 133.5; DB 2; Length 1856;  
Best Local Similarity 35.4%; Pred. No. 0.00019;  
Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;  
QY 8 LATAAARGVEVRALLEAVLPNAPNSYGRRTIQV-MMGSAARVAELLLHGAEPNCAD 66  
DB 507 LHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAAYKGVKRVVAELLLERDAHPNAA 566  
QY 67 PATLTRPVHDAAREGFLDTL-VVLRAGARLDVRDAW-GRLPVDLAELGHRDVARYL-- 122  
DB 567 KNGLT-PLHVAVHHNNLDIVKLLPRGGS--PHSPAANGYTPLHIAAKQNOVEVARSLIQ 623  
QY 123 ---RAAGGTRGSNHARIDAAGPSDI 146  
DB 624 YGGSANAESVQGVTPHLHAAQEGHAEM 650

Search completed: May 7, 2002, 12:33:45  
Job time: 120 sec

RESULT 15  
A35049  
ankyrin 1, erythrocyte splice form 2 - human  
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N:Contains: ankyrin 2.2, erythrocyte  
C:Species: Homo sapiens (man)

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:33:25 ; Search time 11.7 seconds  
(without alignments)  
463.794 Million cell updates/sec

Title: US-09-016-869B-35

Perfect score: 760  
Sequence: 1 MEPSADWLATAAARGRVEEV.....TRGSNHARIDAAEGPSDIPD 148

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	753	99.1	156	1 CDN2_HUMAN	P42771 homo sapien
2	529	69.6	130	1 CDN5_MOUSE	P5271 mus musculus
3	524	68.9	130	1 CDN5_RAT	P5272 rattus norv
4	522	68.7	138	1 CDN5_HUMAN	P42772 homo sapien
5	461.5	60.7	167	1 CDN2_MOUSE	P51480 mus musculus
6	408	53.7	171	1 CDN2_MONDO	O77617 monodelphis
7	259	34.1	166	1 CDN7_HUMAN	P5273 homo sapien
8	249	32.8	166	1 CDN7_MOUSE	Q60773 mus musculus
9	231.5	30.5	168	1 CDN6_MOUSE	Q60772 mus musculus
10	228.5	30.1	168	1 CDN6_HUMAN	P42773 homo sapien
11	158	20.8	3924	1 ANK1_HUMAN	Q01484 homo sapien
12	137.5	18.1	1862	1 ANK1_MOUSE	Q02357 mus musculus
13	133.5	17.6	768	1 YB23_HUMAN	Q9u1j7 homo sapien
14	133.5	17.6	1880	1 ANK1_HUMAN	P16157 homo sapien
15	130.5	17.2	1431	1 DAFK_HUMAN	P53355 homo sapien
16	125	16.4	1059	1 NTC4_MOUSE	P31695 mus musculus
17	123	16.2	1359	1 Y379_HUMAN	O35084 homo sapien
18	118.5	15.6	347	1 GABC_MOUSE	Q00421 mus musculus
19	118.5	15.6	382	1 GABB_MOUSE	Q00420 mus musculus
20	117.5	15.5	347	1 GABC_HUMAN	Q06545 homo sapien
21	117.5	15.5	383	1 GABB_HUMAN	Q06547 homo sapien
22	114	15.0	768	1 BARL_RAT	Q9qzh2 rattus norv
23	114	15.0	2437	1 NOTC_BRARE	P48530 brachydanio
24	111.5	14.7	2531	1 NTC1_RAT	Q07008 rattus norv
25	111	14.6	323	1 ANKH_CHRVI	Q06527 chromatium
26	111	14.6	777	1 BARL_HUMAN	Q99728 homo sapien
27	110.5	14.5	2444	1 NTC1_HUMAN	P46531 homo sapien
28	109.5	14.4	832	1 ANR3_HUMAN	P57078 homo sapien
29	107.5	14.1	2703	1 NOTC_DROME	P07207 drosophila
30	107	14.1	765	1 BARL_MOUSE	O70445 mus musculus
31	104.5	13.8	2524	1 NOTC_XENLA	P21783 xenopus lae
32	103.5	13.6	2318	1 NTC3_MOUSE	Q61982 mus musculus
33	102.5	13.5	740	1 Y050_HUMAN	Q15027 homo sapien

#### RESULT 1

ID	CDN2_HUMAN	STANDARD:	PRT:	156 AA.
AC	P42771; Q15191;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A)			
DE	(MULTIPLE TUMOR SUPPRESSOR 1) (MTS1).			
GN	CDKN2A OR CDKN2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-94081956; PubMed-8259215;			
RA	Serrano M., Hannon G.J., Beach D.;			
RA	"A new regulatory motif in cell-cycle control causing specific			
RT	inhibition of cyclin D/CDK4.";			
RL	Nature 366:704-707(1993).			
RN	[2]			
RP	SEQUENCE OF 51-152 FROM N.A.			
RX	MEDLINE-94204645; PubMed-8153634;			
RA	Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,			
RA	Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,			
RA	Skolnick M.H.;			
RT	"A cell cycle regulator potentially involved in genesis of many tumor			
RT	types.";			
RL	Science 264:436-440(1994).			
RN	[3]			
RP	SEQUENCE OF 1-20 FROM N.A.			
RX	MEDLINE-96182088; PubMed-8622687;			
RA	Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;			
RT	"Regulation of p16CDKN2 expression and its implications for cell			
RT	immortalization and senescence.";			
RL	Mol. Cell. Biol. 16:859-867(1996).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.			
RX	MEDLINE-98421670; PubMed-9751050;			
RA	Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;			
RT	"Structural basis for inhibition of the cyclin-dependent kinase Cdk6			
RT	by the tumour suppressor p16INK4a.";			
RL	Nature 395:237-243(1998).			
RN	[5]			
RP	REVIEW ON MELANOMA VARIANTS.			
RX	MEDLINE-96377761; PubMed-8783570;			
RA	Dracopoli N.C., Fountain J.W.;			
RT	"CDKN2 mutations in melanoma.";			
RL	Cancer Surv. 26:115-132(1996).			
RN	[6]			
RP	REVIEW ON VARIANTS.			
RX	MEDLINE-96303699; PubMed-8723678;			
RA	Smith-Soerensen B., Hovig E.;			
RT	"CDKN2A (p16INK4A) somatic and germline mutations.";			
RL	Hum. Mutat. 7:294-303(1996).			

34	100.5	13.2	414	1	GABD_MOUSE	P81069 mus musculus
35	100.5	13.2	500	1	CACT_DROME	Q03017 drosophila
36	100.5	13.2	1178	1	PH81_YEAST	P17442 saccharomyc
37	99.5	13.1	1454	1	KDGE_DROME	Q09103 drosophila
38	96.5	12.7	571	1	GLS1_CAEEL	Q09103 caenorhabdi
39	96	12.6	679	1	RNSA_MOUSE	Q05921 mus musculus
40	93.5	12.3	227	1	PHLB_SERLI	P18954 serratia li
41	93	12.2	471	1	Y148_HUMAN	Q14161 homo sapien
42	91.5	12.0	2531	1	NTC1_MOUSE	Q01705 mus musculus
43	89	11.7	677	1	SKD3_MOUSE	O60649 mus musculus
44	89	11.7	757	1	HT16_HYDAT	P53356 hydra atten
45	87	11.4	632	1	Y041_HUMAN	Q15057 homo sapien

#### ALIGNMENTS

[7]  
RP VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).  
RX MEDLINE=94338359; PubMed=8060323;  
RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;  
RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41  
cell lung carcinomas.";  
RT cell lung carcinomas.";  
RT Biochem. Biophys. Res. Commun. 202:1426-1430(1994).  
[8]  
RP VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148.  
RX MEDLINE=95078916; PubMed=7987387;  
RA Hussussian C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T.,  
RA Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;  
RT "Germline p16 mutations in familial melanoma.";  
RT Nat. Genet. 8:15-21(1994).  
[9]  
RP VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.  
RX MEDLINE=95060835; PubMed=7970734;  
RA Zhou X., Tarmir L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,  
RA Abraham J.M., Meltzer S.J.;  
RT "The MTS1 gene is frequently mutated in primary human esophageal  
tumors.";  
RT Oncogene 9:3737-3741(1994).  
[10]  
RP VARIANTS.  
RX OKamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,  
RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zarwala M.,  
RA Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;  
RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in  
primary and metastatic lung cancer.";  
RT Cancer Res. 55:1448-1451(1995).  
[11]  
RP VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.  
RX MEDLINE=96121580; PubMed=8959405;  
RA Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M.,  
RA Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;  
RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma  
kindreds.";  
RT Hum. Mol. Genet. 4:1845-1852(1995).  
[12]  
RP CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.  
RX MEDLINE=95375774; PubMed=7647780;  
RA Ranade K., Hussussian C.J., Sikorski R.S., Varmus H.E.,  
RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,  
RA Dracopoli N.C.;  
RT "Mutations associated with familial melanoma impair p16INK4  
function.";  
RT Nat. Genet. 10:114-116(1995).  
[13]  
RP VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.  
RX MEDLINE=96323259; PubMed=8710906;  
RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,  
RA Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,  
RA Iselbacher K.J., Sober A.J., Haber D.A.;  
RT "Prevalence of germ-line mutations in p16, p19ARF, and CDK4 in  
familial melanoma: analysis of a clinic-based population.";  
RT Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).  
[14]  
RP VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.  
RX MEDLINE=97472457; PubMed=9328469;  
RA Harland M., Meloni R., Gruis N., Pinney E., Brookes S., Spurr N.K.,  
RA Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby P.,  
RA Bishop D.T., Bishop J.N.;  
RT "Germline mutations of the CDKN2 gene in UK melanoma families.";  
RT Hum. Mol. Genet. 6:2061-2067(1997).  
[15]  
RP VARIANTS FAMILIAL MELANOMA.  
RX MEDLINE=98087572; PubMed=9425228;  
RA Soufir N., Avril M.-F., Chompret A., Demeunais F., Bombled J.,  
RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;  
RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone  
families in France.";  
RT Hum. Mol. Genet. 7:209-216(1998).  
[16]  
RP ERRATUM.  
RA Soufir N., Avril M.-F., Chompret A., Demeunais F., Bombled J.,  
RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;  
RT Hum. Mol. Genet. 7:941-941(1998).  
[17]  
RP VARIANT PANCREATIC CARCINOMA CYS-146.  
RA Moskaluk C.A., Hruban R.H., Lietman A., Smyrk T., Fusaro L.,  
RA Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.;  
RT "Novel germline p16INK4 allele (Asp145Cys) in a family with multiple  
pancreatic carcinomas.";  
RT Hum. Mutat. 12:70-70(1998).  
[18]  
RP VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.  
RA Gretsardottir S., Olafsdottir G.H., Borg A.;  
RT "Five novel somatic CDKN2/p16 mutations identified in melanoma,  
glioma and carcinoma of the pancreas.";  
RT Hum. Mutat. 12:212-212(1998).  
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS  
CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE  
CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.  
CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.  
CC -1- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A  
CC WIDE RANGE OF TISSUES.  
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
CC INHIBITORS.  
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.  
CC -----  
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CC -----  
DR EMBL; L27211; AAA92554.1; -;  
DR EMBL; U12820; AAB60645.1; -;  
DR EMBL; U12818; AAB60645.1; JOINED.  
DR EMBL; U12819; AAB60645.1; JOINED.  
DR EMBL; S69804; AAD14048.1; -;  
DR EMBL; X94154; CAA63870.1; -;  
DR PDB; 1BI7; 16-FEB-99.  
DR MIM; 600160; -;  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 3.  
DR PROSITE; PS50088; ANK\_REPEAT; FALSE\_NEG.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;  
KW Polymorphism; Li-Fraumeni syndrome; 3D-structure.  
FT REPEAT 11 40 ANK 1.  
FT REPEAT 44 72 ANK 2.  
FT REPEAT 77 106 ANK 3.  
FT REPEAT 110 139 ANK 4.  
FT VARIANT 14 14 D -> E (IN A BILIARY TRACT TUMOR).  
FT FTID=VAR\_001408.  
FT L -> P (IN A BILIARY TRACT TUMOR AND A  
FT FAMILIAL MELANOMA).  
FT FTID=VAR\_001409.  
FT A -> P (IN A LUNG TUMOR AND MELANOMA).  
FT FTID=VAR\_001410.  
FT A -> S (IN A BILIARY TRACT TUMOR).  
FT FTID=VAR\_001411.  
FT G -> D (IN A PANCREAS TUMOR).  
FT FTID=VAR\_001412.  
FT R -> C (IN MELANOMA).  
FT FTID=VAR\_001413.  
FT R -> P (IN FAMILIAL MELANOMA AND  
FT MELANOMA).  
FT FTID=VAR\_001414.  
FT E -> D (IN A BILIARY TRACT TUMOR).  
FT FTID=VAR\_001415.



Query Match 99.1%; Score 753; DB 1; Length 156;  
Best Local Similarity 99.3%; Pred. No. 3.8e-66;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFSADWLATAAARGVEEVRLLEAVALPNAPNSYGRPRIOVMMMGSAARVAELLLHGA 60  
|||||  
Db 9 MFSADWLATAAARGVEEVRLLEAVALPNAPNSYGRPRIOVMMMGSAARVAELLLHGA 68

QY 61 EPNCAOPATITRPVHDAAREGFLDTLVVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 120  
|||||  
Db 69 EPNCAOPATITRPVHDAAREGFLDTLVVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 128

QY 121 YLRAAAGTGRGSHARIDAEGSPDIP 148  
|||||  
Db 129 YLRAAAGTGRGSHARIDAEGSPDIP 156

RESULT 2  
CDN5\_MOUSE STANDARD; PRT; 130 AA.  
AC P55271;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).  
GN CDKN2B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95380169; PubMed=7651726;  
RA Queller D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,  
Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;  
RA "Cloning and characterization of murine p16INK4a and p15INK4b genes.";  
RL Oncogene 11:635-645(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6J X DBA;  
RC MEDLINE=97322242; PubMed=9178896;  
RA Malumbres M., de Castro I., Santos J., Melendez B., Mangueres R.,  
Serrano M., Pellicer A., Fernandez-Piqueras J.;  
RA "Inactivation of the cyclin-dependent kinase inhibitor p15INK4b by  
RT deletion and de novo methylation with independence of p16INK4a  
RT alterations in murine primary T-cell lymphomas.";  
RL Oncogene 14:1361-1370(1997).  
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.  
CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY  
CC SIMILARITY).  
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.  
CC -1- INDUCTION: BY TGF-BETA.  
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
CC INHIBITORS.  
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.  
-----  
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CC -----  
DR EMBL; U66085; AAB39833.1; -;  
DR EMBL; U66084; AAB39833.1; JOINED.  
DR MGD; MGI:104737; Cdkn2b.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 3.  
DR SMART; SM00248; ANK; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.

DR PROSITE; PS50297; ANK\_REPEAT; 1.  
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat.  
FT REPEAT 5 34 ANK 1.  
FT REPEAT 38 66 ANK 2.  
FT REPEAT 71 100 ANK 3.  
FT REPEAT 104 130 ANK 4.  
SQ SEQUENCE 130 AA; 13788 MW; 7AAD60FF552BCFF9 CRC64;

Query Match 69.6%; Score 529; DB 1; Length 130;  
Best Local Similarity 88.3%; Pred. No. 1.5e-44;  
Matches 106; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 8 LATAAAGRVVEVRLLEAVALPNAPNSYGRPRIOVMMMGSAARVAELLLHGAEPNCADP 67  
|||||  
Db 10 LATAAAGRVVEVRLLEAVALPNAPNSYGRPRIOVMMMGSAARVAELLLHGAEPNCADP 69

QY 68 ATLTPVHDAAREGFLDTLVVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 127  
|||||  
Db 70 ATLTPVHDAAREGFLDTLVVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 129

RESULT 3  
CDN5\_MOUSE STANDARD; PRT; 130 AA.  
AC P55272;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).  
GN CDKN2B OR INK4.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96001392; PubMed=7546221;  
RA Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y.,  
Tsuchiya H., Kikuchi Y., Mitani H.;  
RA "Molecular genetic basis of renal carcinogenesis in the Eker rat  
RT model of tuberous sclerosis (Tsc2).";  
RL Mol. Carcinog. 14:23-27(1995).  
RN [2]  
RP SEQUENCE OF 46-86 FROM N.A.  
RX MEDLINE=95228036; PubMed=7712450;  
RA Knaep D.F., Serrano M., Beach D., Trono D., Walker C.L.;  
RA "Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in  
FT kidney epithelial cell lines but not primary renal tumors.";  
RL Cancer Res. 55:1607-1612(1995).  
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.  
CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY  
CC SIMILARITY).  
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.  
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE  
CC INITIATION CODONS IN THE SAME READING FRAME.  
CC -1- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN  
CC TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL  
CC KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.  
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
CC INHIBITORS.  
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.  
-----  
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CC -----  
DR EMBL; S79760; AAB35360.1; -;  
DR EMBL; S77734; -; NOT\_ANNOTATED\_CDS.



```

RP SEQUENCE FROM N.A.
RX MEDLINE=95380169; PubMed=7651726;
RA Ouellet D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.,
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";
RL Oncogene 11:633-645(1995).
CC -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR
CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
CC REGULATORY OF THE PROLIFERATION OF NORMAL CELLS. INHIBITS THE
CC PHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6.
CC -!- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6. PREDOMINANT P16 COMPLEXES
CC CONTAINED CDK6.
CC -!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -!- SIMILARITY: CONTAINS 2 ANK REPEATS.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L76150; AAA85453.1; -.
CC MGD; MGI:104736; Cdkn2a.
CC InterPro: IPR002110; ANK.
CC Pfam; PF00023; ank; 3.
CC SMART; SM00248; ANK; 1.
CC PROSITE; PS50088; ANK_REPEAT; FALSE_NEG.
CC PROSITE; PS50297; ANK_REPEAT; FALSE_NEG.
CC Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
CC CHAIN 1 167
CC CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,
CC LONG ISOFORM.
CC CHAIN 43 167
CC CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,
CC SHORT ISOFORM.
CC INIT_MET 43 43 FOR SHORT ISOFORM.
CC REPEAT 35 63 ANK 1.
CC REPEAT 101 130 ANK 2.
CC SEQUENCE 167 AA; 1780 MW; 88C4588A105ECB8F CRC64;

Query Match 60.7%; Score 461.5; DB 1; Length 167;
Best Local Similarity 63.2%; Pred. No. 6.8e-38;
Matches 98; Conservative 16; Mismatches 32; Indels 9; Gaps 3;

QY 1 MEPSADWLATAAARGVEEVRALLEAVLPNAPNSYGRPIQVMMGMSARVAELLLHGA 60
DB 1 MESAADRLA-RAAQGRVHDVRLLEAGVSPNAPNSFGRTPIQVMMGMSARVAELLLHGA 59
QY 61 EPNCADPATLRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
DB 60 DSNCEDPTTFSPRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 119
QY 121 YLRAA-----AGGT--RGSNRIADAAEGSPDIP 147
DB 120 YLRSAGCSLCSAGWSLCTAGNVAQTGDGHFSFSSSTP 154

RESULT 6
CDN2_MONDO
ID CDN2_MONDO STANDARD; PRT; 171 AA.
AC 077617;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4A)
DE (TUMOR SUPPRESSOR CDKN2A).
GN CDKN2A.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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DR MGD; MGI:105387; Cdkn2d.  
DR InterPro: IPR002110; ANK.  
DR Pfam; PF00023; ank; 3.  
DR SMART; SM00248; ANK; 1.  
DR PROSITE; PS50088; ANK_REPEAT; 1.  
DR PROSITE; PS50297; ANK_REPEAT; 1.  
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; 3D-structure.  
FT REPEAT 73 102 ANK 1.  
FT REPEAT 106 135 ANK 2.  
FT REPEAT 138 166 ANK 3.  
FT REPEAT 17 17 A -> P (IN REF. 2).  
FT CONFLICT 17 17 A -> P (IN REF. 2).  
SQ SEQUENCE 166 AA; 17894 MW; 9E74F5C23B7EBCB2 CRC64;  
  
Query Match 32.8%; Score 249; DB 1; Length 166;  
Best Local Similarity 44.3%; Pred. No. 2.5e-17;  
Matches 70; Conservative 18; Mismatches 52; Indels 18; Gaps 5;  
  
QY 6 DLWATAAARGVEVRALL-EAVALPNAPNSYGRPIQVMMGSAARVAELLHGAEPNC 64  
DB 10 DRLSGARAGDQVRRLLHRELVDPALNRFKGTALQVMMFGSPAVALLELLKQGASPNV 69  
QY 65 ADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAWGRLPVDLAELGHRDVARYL-- 122  
DB 70 QD-ASGTPSVHDAARTGFLDTLVVLRHAGADVNALDSTGSLPIHLAIREGSHSVVSFLAP 128  
QY 123 -----RAAGGT-----RGSNHARIDAEGPSDIP 147  
DB 129 ESDLHHRDASGLTPELARQGAQNL-MDILQGHMMIP 165  
  
RESULT 9  
CDN6_MOUSE STANDARD; PRT; 168 AA.  
AC Q60772;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT  
DE KINASE 4 INHIBITOR C) (P18-INK4C).  
GN CDKN2C.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL KAPLAN;  
RX MEDLINE=95257948; PubMed=7739547;  
RA Hirai H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;  
RT "Novel INK4 proteins, p19 and p18, are specific inhibitors of the  
RT cyclin D-dependent kinases CDK4 and CDK6.";  
RL Mol. Cell. Biol. 15:2672-2681(1995).  
CC -!- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS  
CC CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON  
CC ENDOGENOUS RETINOBLASTOMA PROTEIN RB.  
CC -!- SUBUNIT: HETERODIMER OF P18 WITH CDK6 (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
CC INHIBITORS.  
CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.  
CC -----  
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CC -----  
DR EMBL; U19596; AAC52193.1; -  
DR MGD; MGI:105388; Cdkn2c.  
DR InterPro: IPR002110; ANK.  
DR Pfam; PF00023; ank; 4.  
  
DR SMART; SM00248; ANK; 2.  
DR PROSITE; PS50088; ANK_REPEAT; 2.  
DR PROSITE; PS50297; ANK_REPEAT; 1.  
KW Cell cycle; Repeat; ANK repeat.  
FT REPEAT 4 33 ANK 1.  
FT REPEAT 37 65 ANK 2.  
FT REPEAT 69 98 ANK 3.  
FT REPEAT 102 132 ANK 4.  
FT REPEAT 136 165 ANK 5.  
SQ SEQUENCE 168 AA; 18066 MW; BC88D5489307E128 CRC64;  
  
Query Match 30.5%; Score 231.5; DB 1; Length 168;  
Best Local Similarity 40.3%; Pred. No. 1.3e-15;  
Matches 56; Conservative 22; Mismatches 60; Indels 1; Gaps 1;  
  
QY 2 EPSADWLATAAARGVEVRALLEAVALPNAPNSYGRPIQVMMGSAARVAELLHGAEE 61  
DB 3 EPWGNELASAAAGDLEQLTSLNNVNNVNAQNGFORTALQVMMKGNPIARRLLRGAN 62  
QY 62 PNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAWGRLPVDLAELGHRDVAR 121  
DB 63 PNLKD-GTGEAVTHDAARAGFLDTVQALLEFQADVNIEDNEGNLPLHLAAKSGHLPVVEF 121  
QY 122 LRAAAGTGRGSHARIDAA 140  
DB 122 LMKHTACNVGHRNHKGDTA 140  
  
RESULT 10  
CDN6_HUMAN STANDARD; PRT; 168 AA.  
AC P42773;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT  
DE KINASE 4 INHIBITOR C) (P18-INK4C).  
GN CDKN2C OR CDKN6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95095079; PubMed=8001816;  
RA Guan K., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,  
RA Matera G.A., Xiong Y.;  
RT "Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related  
RT CDK6 inhibitor, correlates with wild-type pRB function.";  
RL Genes Dev. 8:2939-2952(1994).  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANT BREAST CANCER PRO-72.  
RC TISSUE=Breast;  
RX MEDLINE=98300299; PubMed=9636670;  
RA Blais A., Labrie Y., Pouliot F., Lachance Y., Labrie C.;  
RT "Structure of the gene encoding the human cyclin-dependent kinase  
RT inhibitor p18 and mutational analysis in breast cancer.";  
RL Biochem. Biophys. Res. Commun. 247:146-153(1998).  
RN [3]  
RP VARIANT BREAST CANCER PRO-72.  
RX MEDLINE=96438606; PubMed=8840966;  
RA Lapointe J., Lachance Y., Labrie Y., Labrie C.;  
RT "A p18 mutant defective in CDK6 binding in human breast cancer  
RT cells.";  
RL Cancer Res. 56:4586-4589(1996).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).  
RX MEDLINE=98100086; PubMed=9437433;  
RA Venkataramani R., Swaminathan K., Marmorstein R.;  
RT "Crystal structure of the CDK4/6 inhibitory protein p18INK4c provides  
RT insights into ankyrin-like repeat structure/function and  
RT tumor-derived p16INK4 mutations.";
```









RA Cheung M.C., Kan Y.W., Palek J.;  
 RT \*cDNA sequence for human erythrocyte ankyrin.<sup>a</sup>;  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).  
 RN [3]  
 RP VARIANT HS IL-462.  
 RX MEDLINE-96225450; PubMed-8640229;  
 RA Eder S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,  
 RA Dornwell M., Herbers J., Kugler W., Oezcan R., Pektun A.,  
 RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;  
 RA "Ankyrin-1 mutations are a major cause of dominant and recessive  
 RT hereditary spherocytosis";  
 RL Nat. Genet. 13:214-218(1996).  
 CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL  
 CC ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO  
 CC NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE  
 CC CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.  
 CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE  
 CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;  
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC  
 CC PLASMA MEMBRANE.  
 CC -1- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY  
 CC ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN  
 CC VARIANT 2.1.  
 CC -1- PTM: REGULATED BY PHOSPHORYLATION.  
 CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).  
 CC -1- DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE  
 CC HEREDITARY SPHEROCYTOSIS (HS).  
 CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL; X16609; CAA34610.1; -;  
 DR EMBL; M28880; AAA51732.1; -;  
 DR PIR; S08275; SJHUK.  
 DR PIR; A35049; A35049.  
 DR HSP; Q00420; LAWC.  
 DR MIM; 182900; -;  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR000906; ZU5.  
 DR Pfam; PF00023; ank; 23.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00791; ZU5; 1.  
 DR SMART; SM00248; ANK; 22.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00218; ZU5; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 20.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;  
 KW Phosphorylation; Lipoprotein; Multigene family; Disease mutation;  
 KW Elliptocytosis; Polymorphism.  
 FT INIT\_MET 0 0  
 FT DOMAIN 0 1 826 89 KDA DOMAIN (ANTON EXCHANGE PROTEIN  
 FT BINDING DOMAIN).  
 FT DOMAIN 827 1381 62 KDA DOMAIN (SPECTRIN BINDING  
 FT DOMAIN).  
 FT DOMAIN 1382 1880 55 KDA REGULATORY DOMAIN (REGULATES  
 FT THE BINDING OF ANKYRIN TO SPECTRIN  
 FT AND THE BAND 3 PROTEIN).  
 FT REPEAT 43 72 ANK 1.  
 FT REPEAT 76 105 ANK 2.  
 FT REPEAT 109 138 ANK 3.  
 FT REPEAT 142 171 ANK 4.  
 FT REPEAT 173 200 ANK 5.

Query Match 17.6%; Score 133.5; DB 1; Length 1880;  
 Best Local Similarity 35.4%; Pred. No. 6e-05;  
 Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;  
 QY 8 LATAAAGRVVEVRALLEAVLPAPNSYGRPTQV-MMGSAARVAELLLHGAEPNCAD 66  
 Db LHIAAREGHVETVLLALEKEASQACMTKKGFTPLHVAKYGVKVAELLERDHPNAG 565  
 QY 67 PATLTPRVHDAAREGFLDTL-VLHRAAGALRDVRDAW-GRLPVDLAEELGHRDVARYL-- 122  
 Db KGLT-PLHVAVHHNNLDIVKLLPRGSS--PHSPANNGYTPLHIAAKQNVARSILQ 622  
 QY 123 ---RAAGGTGSGNHARIDAAEGPSDI 146  
 Db YGGSANAESVQGVTPHLHAAQGAEM 649  
 RESULT 15  
 DAPK\_HUMAN  
 ID DAPK\_HUMAN STANDARD; PRT; 1431 AA.  
 AC P53355;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).  
 GN DAPK1 OR DAPK.

204 233  
 REPEAT 237 266  
 REPEAT 270 299  
 REPEAT 303 332  
 REPEAT 336 365  
 REPEAT 369 398  
 REPEAT 402 431  
 REPEAT 435 464  
 REPEAT 468 497  
 REPEAT 501 530  
 REPEAT 534 563  
 REPEAT 567 596  
 REPEAT 600 629  
 REPEAT 633 662  
 REPEAT 666 695  
 REPEAT 699 728  
 REPEAT 732 761  
 REPEAT 765 794  
 REPEAT 1402 1486  
 VARSPPLIC 1512 1873  
 VARSPPLIC 1874 1874  
 VARSPPLIC 1849 1880  
 FT REPEAT 204 233  
 FT REPEAT 237 266  
 FT REPEAT 270 299  
 FT REPEAT 303 332  
 FT REPEAT 336 365  
 FT REPEAT 369 398  
 FT REPEAT 402 431  
 FT REPEAT 435 464  
 FT REPEAT 468 497  
 FT REPEAT 501 530  
 FT REPEAT 534 563  
 FT REPEAT 567 596  
 FT REPEAT 600 629  
 FT REPEAT 633 662  
 FT REPEAT 666 695  
 FT REPEAT 699 728  
 FT REPEAT 732 761  
 FT REPEAT 765 794  
 FT REPEAT 1402 1486  
 FT VARSPPLIC 1512 1873  
 FT VARSPPLIC 1874 1874  
 FT VARSPPLIC 1849 1880  
 FT VARIANT 20 20  
 FT VARIANT 462 462  
 FT VARIANT 618 618  
 FT VARIANT 749 749  
 FT VARIANT 844 844  
 FT VARIANT 1285 1285  
 FT VARIANT 1391 1391  
 FT VARIANT 1591 1591  
 FT VARIANT 1698 1698  
 FT CONFLICT 229 229  
 FT CONFLICT 1545 1545  
 FT SEQUENCE 1880 AA; 206145 MW; 1C5F5E7EFD1CD428 CRC64;  
 MISSING (IN ISOFORM 2.2).  
 H -> D (IN ISOFORM 2.2).  
 TVEGLEDPSPSELEVDIDYFMKHSKDTSTNP -> ELRGS  
 GLQPDLLIEGRKGAQIVKRASLKRKQ (IN A THIRD  
 ISOFORM).  
 R -> T.  
 /FTid=VAR\_000595.  
 V -> I (IN HS).  
 /FTid=VAR\_000596.  
 R -> H (IN BRUEGGEN).  
 /FTid=VAR\_000597.  
 V -> A.  
 /FTid=VAR\_000598.  
 D -> E.  
 /FTid=VAR\_000599.  
 E -> D.  
 /FTid=VAR\_000601.  
 S -> T.  
 /FTid=VAR\_000600.  
 D -> N (IN DUESSELDORF).  
 /FTid=VAR\_000602.  
 R -> D.  
 /FTid=VAR\_000603.  
 A -> S (IN REF. 2).  
 V -> I (IN REF. 2).  
 1C5F5E7EFD1CD428 CRC64;

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95129831; PubMed=7828849;  
RA Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;  
RT "Identification of a novel serine/threonine kinase and a novel 15-kD  
RT protein as potential mediators of the gamma interferon-induced cell  
RT death.";  
RL Genes Dev. 9:15-30(1995).  
RN [2]  
RP REVISIONS TO 164-171.  
RA Feinstein E.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL  
CC DEATH.  
CC -!- PTM: AUTOPHOSPHORYLATED.  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC -!- SIMILARITY: CONTAINS 10 ANK REPEATS.  
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
CC -----  
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CC -----  
DR EMBL; X76104; CAA53712.1; .  
DR HSP; O63450; 1A06.  
DR MIM; 600831; .  
DR InterPro: IPR002110; ANK.  
DR InterPro: IPR000488; Death.  
DR InterPro: IPR000719; Ank\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_kin\_actsite.  
DR Pfam: PF00023; ank; 8.  
DR Pfam: PF00531; death; 1.  
DR Pfam: PF00069; pkinase; 1.  
DR SMART; SM00248; ANK; 7.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; 6.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;  
KW Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.  
FT DOMAIN 13 266 PROTEIN KINASE.  
FT DOMAIN 267 334 CALMODULIN-BINDING.  
FT REPEAT 378 407 ANK 1.  
FT REPEAT 411 440 ANK 2.  
FT REPEAT 444 473 ANK 3.  
FT REPEAT 478 507 ANK 4.  
FT REPEAT 511 540 ANK 5.  
FT REPEAT 544 573 ANK 6.  
FT REPEAT 577 606 ANK 7.  
FT REPEAT 610 639 ANK 8.  
FT REPEAT 676 705 ANK 9.  
FT REPEAT 1163 1197 ANK 10.  
FT DOMAIN 1313 1397 DEATH.  
FT NP\_BIND 19 27 ATP (BY SIMILARITY).  
FT BINDING 42 42 BY SIMILARITY).  
FT ACT\_SITE 139 139 BY SIMILARITY.  
FT MUTAGEN 42 42 K->A: LOSS OF ACTIVITY.  
SQ SEQUENCE 1431 AA; 160017 MW; 9EE84811004A155B CRC64;

Query Match

17.2%; Score 130.5; DB 1; Length 1431;

Best Local Similarity 29.1%; Pred. No. 8.6e-05;  
Matches 44; Conservative 14; Mismatches 54; Indels 39; Gaps 4;  
QY 8 LATAAARGVEEVRALLEVALNPAPNSYGRRPQVMMGSR-----VAELLLHGAEPN 63  
DB 483 LHCAAHGYYSVAKALCEAGCNVNKNRGETP---LLTASARGYHDIVECLAEGADLN 539  
QY 64 CADP-----ATL-----TRPVHDAAREGFDTLVVLR 91  
DB 540 ACCKDGHIALHLAVRRQCMVEIKTLLSQGCFVDYQDRHGNTPLHVACKDGNMFIVVALCE 599  
QY 92 AGARLDVRDANGRLPVDIAEELGHRDVARYL 122  
DB 600 ANCNLDISNKYGRTPHLAANNGILDVRYL 630

Search completed: May 7, 2002, 12:36:42  
Job time: 197 sec



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RESULT 2
Q9EQ33 ID Q99PH0 PRELIMINARY; PRT; 157 AA.
AC Q9EQ33;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR 2.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Muscarella P., Knobloch T.J., Weghorst C.M.;
RT "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and
RT Identification of Inactivating Alterations in Hamster Tumor Cell
RT Lines.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF292567; AAG44950.1; -.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 4.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
KW Kinase.
SQ SEQUENCE 157 AA; 16635 MW; 06FD66AE6B30DCFB CRC64;

Query Match 67.1%; Score 510; DB 11; Length 157;
Best Local Similarity 68.9%; Pred. No. 5.7e-37;
Matches 102; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPRPIQVMMGSGARVAEALLLHGA 60
Db 1 MEPSADGLARAAAGQREVRALLEAGVSPNAPNCFGRTPPIQVMMGNTQVARLLLYGA 60
QY 61 EPCNADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVAR 120
Db 61 EPCNEDPATLSRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLALERGHCDVVQ 120
QY 121 YLRAAGGTGRGSHARIDAEGPSDIPD 148
Db 121 YLRAAGNTPGSEPAVTSQAQTPPEVSD 148

RESULT 3
Q99PH0 ID Q99PH0 PRELIMINARY; PRT; 144 AA.
AC Q99PH0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYCLIN-DEPENDENT CELL CYCLE INHIBITOR (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Muscarella P., Knobloch T.J., Weghorst C.M.;
RT "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and
RT Identification of Inactivating Alterations in Hamster Tumor Cell
RT Lines.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF291598; AAG59801.1; -.
DR EMBL; AF291597; AAG59801.1; JOINED.
FT NON_TER 144
SQ SEQUENCE 144 AA; 15206 MW; 8904F9C0C316A084 CRC64;

Query Match 65.9%; Score 501; DB 11; Length 144;
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Best Local Similarity 70.6%; Pred. No. 3.1e-36;
Matches 101; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPRPIQVMMGSGARVAEALLLHGA 60
Db 1 MEPSADGLARAAAGQREVRALLEAGVSPNAPNCFGRTPPIQVMMGNTQVARLLLYGA 60
QY 61 EPCNADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVAR 120
Db 61 EPCNEDPATLSRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLALERGHCDVVQ 120
QY 121 YLRAAGGTGRGSHARIDAEAGP 143
Db 121 YLRAAGNTPGSEPAVTSQAQTP 143

RESULT 4
Q9R0Z3 ID Q9R0Z3 PRELIMINARY; PRT; 159 AA.
AC Q9R0Z3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE P16 PROTEIN P16INK4A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=F344/N; TISSUE=LUNG;
RX MEDLINE=9718461; PubMed=9032263;
RA Swafford D.S., Middleton S.K., Palmisano W.A., Nikula K.J.,
RA Tesfalagi J., Baylín S.B., Herman J.G., Belinsky S.A.;
RT "Frequent aberrant methylation of p16INK4a in primary rat lung
RT tumors.";
RL Mol. Cell. Biol. 17:1366-1374(1997).
DR EMBL; L81167; AAD48924.1; -.
DR HSSP; Q60773; IAP7.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 1.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
SQ SEQUENCE 159 AA; 17366 MW; 3C4CA920A1FEAB6 CRC64;

Query Match 62.7%; Score 476.5; DB 11; Length 159;
Best Local Similarity 74.6%; Pred. No. 4.7e-34;
Matches 97; Conservative 11; Mismatches 19; Indels 3; Gaps 1;

QY 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPRPIQVMMGSGARVAEALLLHGA 60
Db 1 MEPSADGLARAAAGQREVRALLEAGVSPNAPNCFGRTPPIQVMMGNTQVARLLLYGA 60
QY 61 EPCNADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAELGHRDVAR 120
Db 61 DSNCEDPTLSRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLALERGHCDVVR 120
QY 121 YLR---AAAG 127
Db 121 YLRLLSSAG 130

RESULT 5
P97510 ID P97510 PRELIMINARY; PRT; 168 AA.
AC P97510; P97937;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR
DE PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (P16INK4A) (CYCLIN-
DE DEPENDENT KINASE INHIBITOR PROTEIN).
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GN Cdkn2A OR ELALPHA OR p16INK4A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DBA/2N; TISSUE=SPLLEN;  
RX MEDLINE=98151529; PubMed=9482902;  
RA Zhang S., Ramsay E.S., Mock B.A.;  
RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and  
p19ARF, is a candidate for the plasmacytoma susceptibility locus,  
Pctrl.",  
RT Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).  
RN [2]  
RP SEQUENCE OF 1-42 FROM N.A.  
RC STRAIN=VARIOUS STRAINS;  
RX MEDLINE=97179476; PubMed=9021155;  
RA Herzog C.R., You M.;  
RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor  
suppressor gene.",  
RT Mamm. Genome 8:65-66(1997).  
RN [3]  
RP SEQUENCE OF 1-155 FROM N.A.  
RC STRAIN=C57BL/6J X DBA;  
RA Malumbres M., de Castro I., Santos J., Melendez B., Mangues R.,  
Serrano M., Pellicer A., Fernandez-Piqueras J.;  
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 1-42 FROM N.A.  
RC STRAIN=DBA/2, AND C57BL/6;  
RX MEDLINE=95380169; PubMed=7651726;  
RA Quille D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,  
Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;  
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.",  
RN Oncogene 11:635-645(1995).  
RN [5]  
RP SEQUENCE OF 1-42 FROM N.A.  
RC STRAIN=DBA/2, AND C57BL/6;  
RX MEDLINE=97128829; PubMed=8973369;  
RA Soloff E.V., Herzog C.R., You M.;  
RT "The 5'-flanking region of the El alpha form of the murine p16INK4a  
(MTS1) gene.",  
RN Gene 180:213-215(1996).  
RN [7]  
RP SEQUENCE OF 1-42 FROM N.A.  
RC STRAIN=CAST/EI, C57BL/6J, ARF/J, AND MOLF/EI;  
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
Pellicer A., Fernandez-Piqueras J.;  
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
in mouse inbred strains.",  
RN Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF044336; AAC08963.1; -;  
DR EMBL; U49280; AAC00052.1; -;  
DR EMBL; U66087; AAB39600.1; -;  
DR EMBL; U66086; AAB39600.1; JOINED.  
DR EMBL; AF004588; AAB61416.1; -;  
DR EMBL; U47018; AAC52987.1; -;  
DR EMBL; U79628; AAD00226.1; -;  
DR EMBL; U79625; AAD00223.1; -;  
DR EMBL; U79627; AAD00225.1; -;  
DR HSSP; P42771; IBI7.  
DR MGD; MGI:104738; Cdkn2a.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 4.  
DR SMART; SM00248; ANK; 1.  
DR PROSITE; PS50297; ANK\_REP\_REGION; 1.  
KW Kinase; Cyclin.

SQ SEQUENCE 168 AA; 17941 MW; 9A6B0F24F34D5FEC CRC64;  
Query Match 62.6%; Score 476; DB 11; Length 168;  
Best Local Similarity 63.9%; Pred. No. 5.5e-34;  
Matches 99; Conservative 16; Mismatches 32; Indels 8; Gaps 2;  
QY 1 MEPSADWLATAAARGVEVRALLEAVALPNAPNSYGRPRIOVMMGSGARVAEILLHCA 60  
DB 1 MESADRLARAAAGRVHDVRLLEAGVSPNAPNSGFRPTIOVMMGNVHVAALLNLNYGA 60  
QY 61 EPNCAADPATLTPRVHDAAREGEFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120  
DB 61 DSNCEDEPTTFSRPVHDAAREGEFLDTLVVLRHAGARLDVRDAGRLPDLAQRGHQDIVR 120  
QY 121 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 147  
DB 121 YLRSAGCSLCSAGWSLCTAGNVAQTGHSFSSSTP 155  
RESULT 6  
OB9088 ID O89088 PRELIMINARY; PRT; 168 AA.  
AC O89088;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE CYCLIN DEPENDENT KINASE INHIBITOR p16INK4A (p16INK4A TUMOR SUPPRESSOR  
PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).  
DE Cdkn2A OR ELALPHA OR p16.  
GN Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/CANP; TISSUE=SPLEEN;  
RX MEDLINE=98151529; PubMed=9482902;  
RA Zhang S., Ramsay E.S., Mock B.A.;  
RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and  
p19ARF, is a candidate for the plasmacytoma susceptibility locus,  
Pctrl.",  
RT Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).  
RN [2]  
RP SEQUENCE OF 1-42 FROM N.A.  
RC STRAIN=MA/M4J;  
RX MEDLINE=97179476; PubMed=9021155;  
RA Herzog C.R., You M.;  
RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor  
suppressor gene.",  
RN Mamm. Genome 8:65-66(1997).  
RN [3]  
RP SEQUENCE OF 1-42 FROM N.A.  
RC STRAIN=BALB/CJ AND MUS MUS POSCHIAVINUS;  
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
Pellicer A., Fernandez-Piqueras J.;  
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
in mouse inbred strains.",  
RN Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF044335; AAC08962.1; -;  
DR EMBL; U49279; AAC00051.1; -;  
DR EMBL; U79626; AAD00224.1; -;  
DR HSSP; P55273; 1BD8.  
DR MGD; MGI:104738; Cdkn2a.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 4.  
DR SMART; SM00248; ANK; 1.  
DR PROSITE; PS50297; ANK\_REP\_REGION; 1.  
KW Kinase; Cyclin.  
SQ SEQUENCE 168 AA; 17915 MW; 356A973BEAC4D167 CRC64;  
Query Match 62.4%; Score 474; DB 11; Length 168;

Best Local Similarity 63.2%; Pred. No. 8.2e-34;  
Matches 98; Conservative 17; Mismatches 32; Indels 8; Gaps 2;

QY 1 MEPSADWLATAAARGVERVALLCAVALPNAIPNSYGRPPQVMMGSAARVAELLHLHGA 60  
DB 1 MESADRLARAAGQGRVDPVDRALLAGVSPNAPNFGTRTPQVMMGNVHIAALLNLNGA 60  
QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPVDLAELGHRDYAR 120  
DB 61 DSNCEDPTTFSPVHDAAREGFLDTLVVLRHAGARLDVDAWGRLPDLAQERGHQDIVR 120  
QY 121 YLRAA-----AGGT---RGSNHARIDAAEGPSDIP 147  
DB 121 YLRAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP 155

RESULT 7  
Q9XS51 ID Q9XS51 PRELIMINARY; PRT; 102 AA.  
AC Q9XS51;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE P16/CDKN2A/MTS1 (FRAGMENT).  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PBMC;  
RA Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,  
RA Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;  
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)  
and p15(MTS2/CDKN2B).";  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB010807; BAA33540.1; -;  
DR HSSP; P42771; 1B17.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 3.  
DR PROSITE; PS50297; ANK\_REP\_REGION; 1.  
FT NON\_TER 1  
FT NON\_TER 102  
SQ SEQUENCE 102 AA; 10824 MW; 26399FF21359F35D CRC64;

Query Match 59.1%; Score 449; DB 6; Length 102;  
Best Local Similarity 86.0%; Pred. No. 6.7e-32;  
Matches 86; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 43 VMMGSAARVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDAW 102  
DB 1 VMMGSAARVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDAW 60  
QY 103 GRLPVDLAELGHRDVARYLRAAGTGRGSHARIDAAEG 142  
DB 61 GRLPVDLAEEGRHVDIVRYLRARTGGTGSHTGTDGAG 100

RESULT 8  
Q9TSY1 ID Q9TSY1 PRELIMINARY; PRT; 103 AA.  
AC Q9TSY1;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR, P16 (FRAGMENT).  
GN CDKN2A.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=LARGE WHITE;  
RA Le Chalony C., Hayes H., Frelat G., Geffrotin C.;  
RT "Identification and mapping of swine CDKN2A and CDKN2B exon2  
sequences.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ242787; CAB65454.1; -;  
DR HSSP; P42771; 1B17.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 2.  
DR PROSITE; PS50297; ANK\_REP\_REGION; 1.  
KW Kinase; Cyclin.  
FT NON\_TER 1  
FT NON\_TER 103  
SQ SEQUENCE 103 AA; 11023 MW; 5D23ABCC1088DE0B CRC64;

Query Match 58.4%; Score 444; DB 6; Length 103;  
Best Local Similarity 84.3%; Pred. No. 1.8e-31;  
Matches 86; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 43 VMMGSAARVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDAW 102  
DB 1 VMMGSAARVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDAW 60  
QY 103 GRLPVDLAELGHRDVARYLRAAGTGRGSHARIDAAEGPS 144  
DB 61 GRLPVDLAEEGRHVDVAGYLRANARTEGGSHARSNSGEDPA 102

RESULT 9  
Q9XS52 ID Q9XS52 PRELIMINARY; PRT; 86 AA.  
AC Q9XS52;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE P15/MTS2/CDKN2B (FRAGMENT).  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PBMC;  
RA Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,  
RA Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;  
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)  
and p15(MTS2/CDKN2B).";  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB010808; BAA33541.1; -;  
DR HSSP; P55273; 1BD8.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 2.  
DR PROSITE; PS50297; ANK\_REP\_REGION; 1.  
FT NON\_TER 1  
FT NON\_TER 86  
SQ SEQUENCE 86 AA; 9340 MW; A59FF0193290E867 CRC64;

Query Match 56.2%; Score 427; DB 6; Length 86;  
Best Local Similarity 97.6%; Pred. No. 4.5e-30;  
Matches 83; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 43 VMMGSAARVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDAW 102  
DB 1 VMMGSAARVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDAW 60  
QY 103 GRLPVDLAELGHRDVARYLRAAG 127  
DB 61 GRLPVDLAEEGRHVDVARYLRAAG 85

RESULT 10



RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ242788; CAB65455.1; -  
DR HSSP: P55273; 1BD8.  
DR InterPro: IPR002110; ANK.  
DR Pfam: PF00023; ank; 2.  
DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
KW Kinase; Cyclin.  
FT NON\_TER 1  
SQ SEQUENCE 86 AA; 9286 MW; 16EF7A223293CCF9 CRC64;

Query Match 53.6%; Score 407; DB 6; Length 86;  
Best Local Similarity 92.9%; Pred. No. 2.4e-28;  
Matches 79; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 43 VMMSGARVAEELLHGAPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVQDAW 102  
Db 1 VMMSGARVAEELLHGAPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVQDAW 60  
QY 103 GRLPVDLAEELGHRDVARYLRAAG 127  
Db 61 GRLPVDLAEELGHRDVARYLRAAG 85

RESULT 14  
Q54846  
ID O54846 PRELIMINARY; PRT; 86 AA.  
AC O54846;  
DC 01-JUN-1998 (TREMBlrel. 06, Created)  
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15INK4B (FRAGMENT).  
GN CDKN2B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RA Malumbres M., Pellicer A.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF015460; AAB94534.1; -  
DR HSSP: P55273; 1BD8.  
DR InterPro: IPR002110; ANK.  
DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
FT NON\_TER 1  
SQ SEQUENCE 86 AA; 9237 MW; 0499DB26144FB6DF CRC64;

Query Match 53.3%; Score 405; DB 11; Length 86;  
Best Local Similarity 91.8%; Pred. No. 3.6e-28;  
Matches 78; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 43 VMMSGARVAEELLHGAPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVQDAW 102  
Db 1 VMMSGARVAEELLHGAPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVQDAW 60  
QY 103 GRLPVDLAEELGHRDVARYLRAAG 127  
Db 61 GRLPVDLAEELGHRDVARYLRAAG 85

RESULT 15  
Q921C2  
ID Q921C2 PRELIMINARY; PRT; 113 AA.  
AC Q921C2;  
DC 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
GN P16.  
OS Mus spretus (Western wild mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10096;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRET/EI;  
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
RA Pellicer A., Fernandez-Piqueras J.;  
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
in mouse inbred strains.";  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U79634; AAD00236.1; -  
DR HSSP: P55273; 1BD8.  
DR InterPro: IPR002110; ANK.  
DR Pfam: PF00023; ank; 2.  
DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
KW Kinase; Cyclin.  
FT NON\_TER 1  
FT NON\_TER 113  
SQ SEQUENCE 113 AA; 12073 MW; C3BFE8325DB2D79E CRC64;

Query Match 43.9%; Score 334; DB 11; Length 113;  
Best Local Similarity 61.1%; Pred. No. 7.1e-22;  
Matches 69; Conservative 12; Mismatches 24; Indels 8; Gaps 2;

QY 43 VMMSGARVAEELLHGAPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVQDAW 102  
Db 1 VMMSGARVAEELLHGAPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVQDAW 60  
QY 103 GRLPVDLAEELGHRDVARYLRAA-----AGGT--RGSNHARIDAAEGPSDIP 147  
Db 61 GRLPDLAQERGHQDIVRYLRSAGCSLCSAGWSLCTAGNVAQTGHSFSSSTP 113

Search completed: May 7, 2002, 12:36:23  
Job time: 193 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:23:49 ; Search time 23.63 Seconds  
(without alignments)  
463.938 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 760

Sequence: 1 MEPSADNLATAAARGVEEV.....TRGSNHNARIDAERGSPDIPD 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_1101.\*

- 1: /SIDSB/gcgdata/geneseq/geneseq/AA1980.DAT.\*
- 2: /SIDSB/gcgdata/geneseq/geneseq/AA1981.DAT.\*
- 3: /SIDSB/gcgdata/geneseq/geneseq/AA1982.DAT.\*
- 4: /SIDSB/gcgdata/geneseq/geneseq/AA1983.DAT.\*
- 5: /SIDSB/gcgdata/geneseq/geneseq/AA1984.DAT.\*
- 6: /SIDSB/gcgdata/geneseq/geneseq/AA1985.DAT.\*
- 7: /SIDSB/gcgdata/geneseq/geneseq/AA1986.DAT.\*
- 8: /SIDSB/gcgdata/geneseq/geneseq/AA1987.DAT.\*
- 9: /SIDSB/gcgdata/geneseq/geneseq/AA1988.DAT.\*
- 10: /SIDSB/gcgdata/geneseq/geneseq/AA1989.DAT.\*
- 11: /SIDSB/gcgdata/geneseq/geneseq/AA1990.DAT.\*
- 12: /SIDSB/gcgdata/geneseq/geneseq/AA1991.DAT.\*
- 13: /SIDSB/gcgdata/geneseq/geneseq/AA1992.DAT.\*
- 14: /SIDSB/gcgdata/geneseq/geneseq/AA1993.DAT.\*
- 15: /SIDSB/gcgdata/geneseq/geneseq/AA1994.DAT.\*
- 16: /SIDSB/gcgdata/geneseq/geneseq/AA1995.DAT.\*
- 17: /SIDSB/gcgdata/geneseq/geneseq/AA1996.DAT.\*
- 18: /SIDSB/gcgdata/geneseq/geneseq/AA1997.DAT.\*
- 19: /SIDSB/gcgdata/geneseq/geneseq/AA1998.DAT.\*
- 20: /SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT.\*
- 21: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT.\*
- 22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	760	100.0	148	16	Multiple tumour su
2	760	100.0	148	16	Human multiple tum
3	760	100.0	151	15	Inhibitor of cycli
4	760	100.0	156	16	Cell-cycle regulat
5	760	100.0	156	20	Human INK-4 protei
6	760	100.0	156	21	Human cell cycle r
7	760	100.0	391	18	CDK inhibitory fus
8	760	100.0	391	20	Human p27-pl6 fusi
9	760	100.0	391	21	Human W3 protein s
10	760	100.0	391	21	Antiproliferative
11	760	100.0	391	21	Angiogenesis inhib

12	753	99.1	156	18	AAW10627	Tumour suppressor
13	753	99.1	156	18	AAW19251	Human multiple tum
14	753	99.1	156	19	AAW74549	Amino acid sequenc
15	753	99.1	156	19	AAW40524	Human WTS1 protein
16	753	99.1	156	20	AAW80524	A human multiple t
17	753	99.1	156	21	AAW15498	Human WTS1 protein
18	753	99.1	156	21	AAW97524	Human p16 protein
19	753	99.1	156	21	AAW96053	Human cyclin depen
20	753	99.1	156	21	AAW96067	Human cyclin depen
21	753	99.1	156	21	AAW92921	Human multiple tum
22	753	99.1	156	21	AAW91102	Human multiple tum
23	753	99.1	156	21	AAW59415	Human WTS1 protein
24	753	99.1	156	21	AAW54902	Human multiple tum
25	753	99.1	156	22	AAW02122	Human multiple tum
26	753	99.1	156	22	AAE01002	Human multiple tum
27	753	99.1	156	22	AAW67334	Protein encoded by
28	753	99.1	156	22	AAW36890	Human Multiple Tum
29	753	99.1	228	21	AAW97522	Human W9 protein s
30	753	99.1	228	21	AAW96051	Antiproliferative
31	753	99.1	228	21	AAW96078	Angiogenesis inhib
32	753	99.1	237	20	AAW95105	Truncated p27/p16
33	753	99.1	237	21	AAW97534	Human W9 protein s
34	753	99.1	237	21	AAW96049	Antiproliferative
35	753	99.1	237	21	AAW96076	Angiogenesis inhib
36	753	99.1	252	20	AAW95106	Truncated p27/p16
37	753	99.1	252	21	AAW97535	Human W10 protein
38	753	99.1	252	21	AAW96050	Antiproliferative
39	753	99.1	252	21	AAW96077	Angiogenesis inhib
40	753	99.1	323	21	AAW96079	Secretable angio
41	753	99.1	334	20	AAW95103	Truncated p27/p16
42	753	99.1	334	21	AAW97532	Human W8 protein s
43	753	99.1	334	21	AAW96047	Antiproliferative
44	753	99.1	334	21	AAW96074	Angiogenesis inhib
45	753	99.1	365	18	AAW23536	CDK inhibitory fus

ALIGNMENTS

RESULT 1

AAW1701

ID AAR81701 standard; Protein; 148 AA.

XX AAR81701;

AC AAR81701;

DT 08-MAY-1996 (first entry)

DE Multiple tumour suppressor 1 (MTS1) polypeptide.

DE Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;

DE predisposition; melanoma; leukaemia; lymphoma; prognosis;

DE pancreas; breast; thyroid.

XX Homo sapiens.

XX WO9525813-A1.

PN 28-SEP-1995.

PD 17-MAR-1995; 95WO-US03537.

XX 01-JUN-1994; 94US-0251938.

PR 18-MAR-1994; 94US-0214582.

PR 18-MAR-1994; 94US-0215086.

PR 14-APR-1994; 94US-0227369.

XX (MYRI-) MYRIAD GENETICS INC.

PA (UTAH) UNIV UTAH RES FOUND.

XX Cannon-Albright LA, Kamb A, Skolnick MH;

XX WPI; 1995-344626/44.

DR N-PSDB; AAT00736.  
 XX Detecting polymorphism associated with cancer pre-disposition - also  
 PT DNA, vectors and host cells e.g. for gene or protein replacement  
 PT therapy and drug screening  
 XX  
 PS Example 8; Pages 92-93; 148pp; English.  
 XX  
 CC An individual can be diagnosed as having a predisposition to cancer  
 CC by detecting an alteration in the wild type multiple tumour  
 CC suppressor (MTS) gene, using gene probes which hybridise to the MTS1  
 CC gene ORF AAT00736 (which encodes AAR81701) mutant sequences AAT00749/50.  
 CC The above assay can also be used in the diagnosis and prognosis of  
 CC melanoma, lymphoma, leukaemia and pancreas, breast and thyroid  
 CC cancers, etc..  
 XX  
 SQ Sequence 148 AA;  
 Query Match 100.0%; Score 760; DB 16; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-83;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPIQVMMGMSARVAELLLHGA 60  
 DB 1 mepsadwlataaargveevrallleavalpnapsygrpiqvmmsarvae1lllhga 60  
 QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRAGRLPVDLAEEELGHRDVAR 120  
 DB 61 epncadpatltrpvhdaaregfdtlvvlhragardlvdragrlpvdlaeeighrdvar 120  
 QY 121 YLRAAAGGTRGSHARIDAAEGPSDIPD 148  
 DB 121 ylraaaggtrgsharidaaegpsdipd 148  
 RESULT 2  
 ID AAR80940 standard; Protein; 148 AA.  
 XX AAR80940;  
 XX  
 DT 03-MAY-1996 (first entry)  
 XX  
 DE Human multiple tumour suppressor polypeptide, MTS1.  
 XX  
 KW Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;  
 KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;  
 KW gene therapy; chronic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9525429-A1.  
 XX  
 PD 28-SEP-1995.  
 XX  
 PF 17-MAR-1995; 95WO-US03316.  
 XX  
 PR 01-JUN-1994; 94US-0251938.  
 PR 18-MAR-1994; 94US-0214581.  
 PR 18-MAR-1994; 94US-0214582.  
 PR 18-MAR-1994; 94US-0215088.  
 PR 14-APR-1994; 94US-0227369.  
 PR 18-MAR-1994; 94US-0215086.  
 PR 18-MAR-1994; 94US-0215087.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX  
 PI Kamb A;  
 XX  
 DR WPI; 1995-344401/44.  
 DR N-PSDB; AAQ99158.  
 XX

PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences  
 PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.  
 PT melanoma or leukaemia  
 XX  
 PS Claim 5; Page 92-93; 156pp; English.  
 XX  
 CC Several multiple tumour suppressor (MTS) polypeptides have been  
 CC isolated and sequenced. This sequence is the MTS polypeptide MTS1  
 CC MTS polypeptide-encoding cDNAs and mutants of these are useful for  
 CC the diagnosis or prognosis of human cancer. Germ-line mutations of  
 CC MTS cDNAs can be used for diagnosing predisposition to melanoma,  
 CC leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's  
 CC lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus,  
 CC testis, kidney, stomach and rectum. The wild-type gene is useful  
 CC for gene therapy and MTS polypeptides may also be used for protein  
 CC replacement therapy. Also the polypeptides or cells contg. an  
 CC altered MTS gene are useful for screening for potential cancer  
 CC therapeutics.  
 XX  
 SQ Sequence 148 AA;  
 Query Match 100.0%; Score 760; DB 16; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-83;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRPIQVMMGMSARVAELLLHGA 60  
 DB 1 mepsadwlataaargveevrallleavalpnapsygrpiqvmmsarvae1lllhga 60  
 QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRAGRLPVDLAEEELGHRDVAR 120  
 DB 61 epncadpatltrpvhdaaregfdtlvvlhragardlvdragrlpvdlaeeighrdvar 120  
 QY 121 YLRAAAGGTRGSHARIDAAEGPSDIPD 148  
 DB 121 ylraaaggtrgsharidaaegpsdipd 148  
 RESULT 3  
 ID AAR53401 standard; Protein; 151 AA.  
 XX AAR53401;  
 XX  
 DT 07-DEC-1994 (first entry)  
 XX  
 DE Inhibitor of cyclin dependent kinase 4 (p16INK4).  
 XX  
 KW Cyclin; cyclin dependent kinase; CDK; oncogene; cancer; leukaemia;  
 KW lymphoma; cell cycle; detection; identification; tumour virus;  
 KW proliferating cell nuclear antigen; subunit; complex.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9409135-A.  
 XX  
 PD 28-APR-1994.  
 XX  
 PF 18-OCT-1993; 93WO-US09945.  
 XX  
 PR 16-OCT-1992; 92US-0963308.  
 PR 17-DEC-1992; 92US-0991997.  
 XX  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 XX  
 PI Beach DH, Xiong Y;  
 XX  
 DR WPI; 1994-151320/18.  
 DR N-PSDB; AAQ63491.  
 XX  
 PT Detection of subunit components of cyclin complexes - used for  
 PT diagnosing transformation of a cell and developing inhibitors and





```

FT XX /note= *(Gly4Ser)2 linker"
FN XX
XX KW W09727297-A1.
XX KW
XX PD 31-JUL-1997.
XX KW
XX PF 17-JAN-1997; 97WO-US00569.
XX KW
XX PR 23-JAN-1996; 96US-0589981.
XX OS
XX PA (MITO-) MITOTIX INC.
XX PI Beach D, Gyuris J, Lamphere L;
XX PR WPI; 1997-393685/36.
XX DR N-PSDB; AAT74051.
XX KW
XX PT Chimeric inhibitor of cyclin dependent kinase - useful for gene
XX PT therapy of cancer and other proliferative and differentiative
XX PT diseases
XX KW
XX PS Claim 40; Page 38-40; 58pp; English.
XX CC
XX CC This sequence represents a chimeric polypeptide of the invention. It was
XX CC derived from a fusion of the human p27 and p16 cDNA sequences. The
XX CC chimeric polypeptides of the invention have cyclin-dependent kinase (CDK)
XX CC binding motifs from at least two different proteins that bind to CDKs.
XX CC The protein controls proliferation and/or differentiation of cells,
XX CC particularly they inhibit cell-cycle progression. They can be used to
XX CC treat a wide range of proliferative disorders, e.g. cancer, leukaemia,
XX CC psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They
XX CC can also treat diseases associated with de-differentiation or
XX CC degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's
XX CC diseases, gastric ulcers and autonomous diseases of the peripheral
XX CC nervous system. Other applications include reducing growth of hair and
XX CC protecting hair follicle cells against cytotoxic treatments, cosmetically
XX CC to treat various forms of folliculitis, and to inhibit spermatogenesis or
XX CC oogenesis. The chimeric proteins can also be used in vitro to maintain
XX CC cells, especially neurons intended for testing specific activity of
XX CC trophic factors, at selected points in the cell cycle. The proteins are
XX CC more active inhibitors of the CDK/cyclin complex than binding motifs used
XX CC individually (since they may bind to CDK involved in different stages of
XX CC the cell cycle).
XX SQ Sequence 391 AA;

Query Match 100.0%; Score 760; DB 18; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.6e-82;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLATAAARGRVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAELLHGA 60
|||||
Db 244 mepsadwlataaargrveevrralleavalpnapsygrrrpqvmngmsarvae||llhga 303
|||||
Qy 61 EPNCADPATLRPVHDAARSGFDLTLLVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 120
|||||
Db 304 epcnacadpatlrpvhdaregfdltllvlhragardldvdrdagrplpvdlaeelghrdvar 363
|||||
Qy 121 YLRAAGGTGCSNHARTDAAGPSDIPD 148
|||||
Db 364 ylraaggtgrgsharidaagpsdipd 391
|||||

RESULT 8
AAW95094
ID AAW95094 standard; Protein; 391 AA.
AC AAW95094;
XX
XX 25-MAY-1999 (first entry)
XX
XX Human p27-p16 fusion protein.

```

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XX KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
XX KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
XX KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
XX KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
XX KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
XX KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
XX KW tachycardia; human; p27; p16.
XX OS
XX PA Homo sapiens.
XX PN W09906540-A2.
XX XX
XX PD 11-FEB-1999.
XX XX
XX PF 29-JUL-1998; 98WO-US15759.
XX XX
XX PR 29-JUL-1997; 97US-0902572.
XX XX
XX PA (MITO-) MITOTIX INC.
XX PI Beach DH, Gyuris J, Lamphere L;
XX XX
XX DR WPI; 1999-153770/13.
XX DR N-PSDB; AAX26220.
XX XX
XX PT Fusion and chimaeric proteins including cyclin-dependent kinase
XX PT binding motif - used for regulation of cell proliferation and
XX PT differentiation, for treatment of, e.g. vascular injury, cancers,
XX PT fibrosis and neurodegeneration
XX PS Claim 63; Page 70-72; 88pp; English.
XX CC
XX CC The invention relates to novel inhibitors of cyclin-dependent kinases
XX CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
XX CC transfection system (A) that comprises: (i) first gene construct
XX CC comprising a sequence encoding an inhibitory polypeptide containing at
XX CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
XX CC linked to a transcription regulator functional in eukaryotic cells; (ii)
XX CC second gene construct comprising a sequence encoding a polypeptide that
XX CC promotes endothelialisation, and (iii) a gene delivery composition for
XX CC delivering the GCS to a cell for transfection. Also provided are nucleic
XX CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
XX CC polypeptide sequence (TP) from an intracellular protein that alters a
XX CC cellular process when FP enters the cell, and (ii) a transcellular
XX CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
XX CC consists of at least one CDK-binding motif and a TCP. (A) are used to
XX CC treat vascular wounds that involve a break in the endothelium and
XX CC excessive proliferation of smooth muscle, particularly restenosis but
XX CC more generally any repair of cardiovascular damage, arteriosclerotic
XX CC lesions or for endothelialisation of synthetic vascular grafts. More
XX CC generally, FP are used to treat unwanted cellular proliferation in a very
XX CC wide range of situations, e.g. for treating vascular diseases as above;
XX CC fibrotic disorders (e.g. rheumatoid arthritis, diabetes, cirrhosis); many
XX CC tumours (gliomas, leukaemias); chronic inflammation; neurodegeneration;
XX CC acne; also to control hair growth (e.g. to prevent hair loss caused by
XX CC chemotherapy or radiation); periodontal disease; to treat tachycardia;
XX CC to inhibit spermatogenesis etc. Chimaeric proteins comprising CDK-binding
XX CC motifs from two or more different proteins bind to CDKs so inhibit cell
XX CC cycle progression, particularly smooth muscle cell proliferation. The
XX CC gene constructs may also be used to produce FP in cell cultures, for
XX CC production or for regulating cell differentiation in vitro. The present
XX CC sequence represents a human p27-p16 fusion protein.
XX SQ Sequence 391 AA;

```

Query Match 100.0%; Score 760; DB 20; Length 391;

Best Local Similarity 100.0%; Pred. No. 1.6e-82;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLATAAARGRVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAELLHGA 60  
 |||||||



CC by injury caused by angioplasty, stent placement or vein  
 CC engraftment. It is useful for treating vascular pathologies e.g.,  
 CC restenosis. Also claimed are recombinant lentiviruses encoding  
 CC CDKis.  
 XX  
 SQ Sequence 391 AA;

Query Match 100.0%; Score 760; DB 21; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-82;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQVMMGMSARVAELLHLHGA 60  
 DB 244 mepsadwlataaargveevrllleavlpnapnsygrripqvmgmgsarvaeillhlhga 303  
 QY 61 EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRAGRLPVDLAEEIGHRDVAR 120  
 DB 304 epcnccadpatltprvhdaaregfldtlvvlhragardlvdrdgrlpvdlaeelghrdvar 363  
 QY 121 YLRAAAGTGRGSHNARIDAAEGPSDIPD 148  
 DB 364 ylraaagtgtrgshnaridaaegpsdipd 391

RESULT 11  
 AAY96068  
 ID AAY96068 standard; Protein; 391 AA.  
 AC AAY96068;  
 XT 05-DEC-2000 (first entry)  
 DE Angiogenesis inhibitor (p27-p16 fusion) W3.  
 XX  
 KW Cyclin dependent kinase inhibitor; CDK; CIP; KIP; INK4; p27; p16;  
 KW human; angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
 KW endometriosis; psoriasis; vascular retinopathy; cytostatic;  
 KW antiarthritic; antirheumatic; gynaecological; antipsoriatic;  
 KW antiproliferative; gene therapy.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX

Key Location/Qualifiers  
 FH Peptide 1..7  
 FT /label= 6His\_tag  
 FT Protein 8..204  
 FT /label= p27  
 FT Peptide 205..219  
 FT /label= Hinge  
 FT Protein 239..391  
 FT /label= p16  
 XX  
 PN WO200052158-A1.  
 XX  
 PD 08-SEP-2000.  
 XX  
 PF 28-FEB-2000; 2000WO-US04970.  
 XX  
 PR 01-MAR-1999; 99US-0122974.  
 PR 05-NOV-1999; 99US-0163682.  
 PR 09-DEC-1999; 99US-0457646.  
 XX  
 XX (CELL-) CELL GENESYS INC.  
 PA (MITO-) MITOTIX INC.  
 PA  
 XX Patel S, Mearthur J, Gyuris J;  
 XX  
 DR WPI; 2000-565501/52.  
 DR N-PSDB; AAA50523.  
 XX  
 PT Inhibiting angiogenesis and treating angiogenesis-associated

PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial  
 PT cell with a recombinant virus having a transgene encoding a cyclin  
 XX dependent kinase inhibitor  
 PS Example 1; Page 108-110; 138pp; English.  
 XX  
 CC The present sequence is that of p27-p16 fusion protein W3  
 CC comprising an N-terminal 6His tag, the human p27 protein (see  
 CC AAY96066), a (Gly4Ser)3 hinge, and the human p16 protein (see  
 CC AAY96067). The fusion protein is encoded by a nucleic acid (see  
 CC AAA50523) that was obtained by PCR amplification of human p27 and p16  
 CC DNAs using primers that also included codons encoding the tag/hinge  
 CC regions of the fusion protein. A claimed method for inhibiting  
 CC angiogenesis involves transducing an epithelial cell with a  
 CC transgene encoding a cell dependent kinase inhibitor (CDK). The  
 CC delivery system for the transgene is a liposome or a recombinant  
 CC virus. The CDK1 is a protein of the CIP/KIP family such as p27, a  
 CC protein of the INK4 family such as p16, active fragments of these  
 CC proteins, or a fusion of 2 CDK1 proteins such as p27 and p16. The  
 CC method is useful in treating conditions associated with angiogenesis,  
 CC such as neoplasia, rheumatoid arthritis, endometriosis, psoriasis  
 CC and vascular retinopathy (claimed). Alternatively, the transgene  
 CC is delivered to an auxiliary cell, and is expressed by that cell  
 CC such that the CDK1 is released into the blood and contacts the  
 CC target epithelial cell. The p27-p16 fusion proteins interact with  
 CC CDK4/cyclinD, CDK2/cyclinA and CDK2/cyclinE and inhibit cell cycle  
 CC progression.  
 XX Sequence 391 AA;

Query Match 100.0%; Score 760; DB 21; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-82;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQVMMGMSARVAELLHLHGA 60  
 DB 244 mepsadwlataaargveevrllleavlpnapnsygrripqvmgmgsarvaeillhlhga 303  
 QY 61 EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRAGRLPVDLAEEIGHRDVAR 120  
 DB 304 epcnccadpatltprvhdaaregfldtlvvlhragardlvdrdgrlpvdlaeelghrdvar 363  
 QY 121 YLRAAAGTGRGSHNARIDAAEGPSDIPD 148  
 DB 364 ylraaagtgtrgshnaridaaegpsdipd 391

RESULT 12  
 AAW10627  
 ID AAW10627 standard; Protein; 156 AA.  
 AC AAW10627;  
 XX  
 XX 28-OCT-1997 (first entry)  
 DT Tumour suppressor p16.  
 XX  
 XX Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;  
 KW cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;  
 KW anti-angiogenic activity; hyperproliferative disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9703635-A2.  
 XX  
 PD 06-FEB-1997.  
 XX  
 PF 17-JUL-1996; 96WO-US11787.  
 XX  
 PR 17-JUL-1995; 95US-0502881.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.





DR WPI; 1998-494842/42.  
 DR N-PSDB; AAV53819.  
 XX  
 PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -  
 PT useful as hybridisation probes, primers and recombinant production  
 PT of MTS in the diagnosis and treatment of cancers related to MTS  
 PT mutation(s)  
 XX  
 PS Disclosure; Column 63-64; 73pp; English.  
 XX  
 CC This is the amino acid sequence of the multiple tumour suppressor 1  
 CC (MTS-1) protein, used in the method of the invention. The MTS gene  
 CC is useful in the diagnosis and prognosis of human cancer, e.g. by  
 CC standard nucleic hybridisation techniques, of patient samples. The  
 CC mutated sequences are those that are present in somatic mutations  
 CC of the gene in cancers. The vectors can be used for gene therapy  
 CC strategies to replace function of mutated protein in patients. These  
 CC can also be used to construct protein mimetics, also for therapeutic  
 CC strategies. In addition the expression constructs can also be used  
 CC for recombinant production of MTS. Recombinant MTS can be used to  
 CC screen for drugs to be used for cancer therapy, and the protein  
 CC itself may also be used to restore MTS function in a cell.  
 XX  
 SQ Sequence 156 AA;

Query Match 99.1%; Score 753; DB 19; Length 156;  
 Best Local Similarity 99.3%; Pred. No. 3.3e-82;  
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPRPIQYMMGSAFVAELLLHGA 60  
 DB 9 mepsadwlataaargveevrallleagalpnapsygrprpiqymmggsarvaeillllhga 68  
 QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120  
 DB 69 epncadpatltrpvhdaaregfdtlvvlrhagarldvrdawgrlpvdlaeelghrdvar 128  
 QY 121 YLRAAAGGTGRGSHNARIDAAEGPSDIPD 148  
 DB 129 yltraaaggtgrgshnaridaaegpsdipd 156

RESULT 15  
 AAW40524  
 ID AAW40524 standard; Protein; 156 AA.  
 XX  
 AC AAW40524;  
 XX  
 DT 15-JUL-1998 (first entry)  
 XX  
 DE Human MTS1 protein.  
 XX  
 KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;  
 KW familial melanoma locus; MLM; predisposition.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5739027-A.  
 XX  
 PD 14-APR-1998.  
 XX  
 PF 07-JUN-1995; 95US-0487033.  
 XX  
 PR 07-JUN-1995; 95US-0487033.  
 PR 18-MAR-1994; 94US-0214582.  
 PR 18-MAR-1994; 94US-0215086.  
 PR 18-MAR-1994; 94US-0215087.  
 PR 14-APR-1994; 94US-0227369.  
 PR 01-JUN-1994; 94US-0251938.  
 PR 17-MAR-1995; 95WO-US03316.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.

XX Kamb A;  
 PI  
 XX WPI; 1998-250421/22.  
 DR N-PSDB; AAV11238.  
 XX  
 PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are  
 PT useful for the diagnosis of cancers related to MTS1E1-beta  
 PT mutation(s) and their treatment  
 XX  
 PS Disclosure; Column 63-64; 72pp; English.  
 XX  
 CC This sequence represents a human multiple tumour suppression protein,  
 CC MTS1. The MTS gene locus is also referred to as the familial melanoma  
 CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations  
 CC in MTS genes can be used in the diagnosis of predisposition to cancers,  
 CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,  
 CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,  
 CC ovary, uterus, testis, kidney, stomach and rectum.  
 XX  
 SQ Sequence 156 AA;

Query Match 99.1%; Score 753; DB 19; Length 156;  
 Best Local Similarity 99.3%; Pred. No. 3.3e-82;  
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPRPIQYMMGSAFVAELLLHGA 60  
 DB 9 mepsadwlataaargveevrallleagalpnapsygrprpiqymmggsarvaeillllhga 68  
 QY 61 EPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120  
 DB 69 epncadpatltrpvhdaaregfdtlvvlrhagarldvrdawgrlpvdlaeelghrdvar 128  
 QY 121 YLRAAAGGTGRGSHNARIDAAEGPSDIPD 148  
 DB 129 yltraaaggtgrgshnaridaaegpsdipd 156

Search completed: May 7, 2002, 12:33:04  
 Job time: 555 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:32:10 ; Search time 105.99 Seconds  
(without alignments)  
490.476 Million cell updates/sec

Title: US-09-016-869B-35  
Perfect score: 760  
Sequence: 1 MEPSADWLATAAARGVEEV.....TRGSNHARIDAEGPSDIPD 148

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3516493 seqs, 351254056 residues

Total number of hits satisfying chosen parameters: 3516493

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

- 1: /cgn2\_6/ptodata/2/paa/pctus\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US080\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/paa/US082\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/2/paa/US083\_COMB.pep.\*
- 8: /cgn2\_6/ptodata/2/paa/US084\_COMB.pep.\*
- 9: /cgn2\_6/ptodata/2/paa/US085\_COMB.pep.\*
- 10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep.\*
- 11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep.\*
- 12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep.\*
- 13: /cgn2\_6/ptodata/2/paa/US089\_COMB.pep.\*
- 14: /cgn2\_6/ptodata/2/paa/US090\_COMB.pep.\*
- 15: /cgn2\_6/ptodata/2/paa/US091\_COMB.pep.\*
- 16: /cgn2\_6/ptodata/2/paa/US092\_COMB.pep.\*
- 17: /cgn2\_6/ptodata/2/paa/US093\_COMB.pep.\*
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- 19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep.\*
- 20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep.\*
- 21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep.\*
- 22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*
- 23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep.\*
- 24: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*
- 25: /cgn2\_6/ptodata/2/paa/US60\_MERGED\_COMB.pep1.\*
- 26: /cgn2\_6/ptodata/2/paa/US10\_MERGED\_COMB.pep1.\*
- 27: /cgn2\_6/ptodata/2/paa/US09\_MERGED\_COMB.pep2.\*
- 28: /cgn2\_6/ptodata/2/paa/US09\_MERGED\_COMB.pep1.\*
- 29: /cgn2\_6/ptodata/2/paa/US08\_MERGED\_COMB.pep1.\*
- 30: /cgn2\_6/ptodata/2/paa/US07\_MERGED\_COMB.pep1.\*
- 31: /cgn2\_6/ptodata/2/paa/US06\_MERGED\_COMB.pep1.\*
- 32: /cgn2\_6/ptodata/2/paa/PCT\_MERGED\_COMB.pep1.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	760	100.0	148	1	PCT-US95-03316-2 Sequence 2, Appli

1	PCT-US95-03537-2	148	760	100.0	148	Sequence 2, Appli
6	US-08-214-581-2	148	760	100.0	148	Sequence 2, Appli
6	US-08-214-582-2	148	760	100.0	148	Sequence 2, Appli
6	US-08-215-086-2	148	760	100.0	148	Sequence 2, Appli
6	US-08-215-087-2	148	760	100.0	148	Sequence 2, Appli
6	US-08-215-088-2	148	760	100.0	148	Sequence 2, Appli
6	US-08-227-369-2	148	760	100.0	148	Sequence 2, Appli
6	US-08-227-371-2	148	760	100.0	148	Sequence 2, Appli
18	US-09-480-135-16	148	760	100.0	148	Sequence 16, Appli
18	US-09-480-135-24	148	760	100.0	148	Sequence 24, Appli
28	US-09-016-869B-35	148	760	100.0	148	Sequence 35, Appli
6	US-08-248-812-2	156	760	100.0	156	Sequence 2, Appli
7	US-08-306-511-2	156	760	100.0	156	Sequence 2, Appli
8	US-08-497-214A-2	156	760	100.0	156	Sequence 2, Appli
8	US-08-497-214B-2	156	760	100.0	156	Sequence 2, Appli
8	US-08-497-214C-2	156	760	100.0	156	Sequence 2, Appli
8	US-08-497-214D-2	156	760	100.0	156	Sequence 2, Appli
9	US-08-581-918-2	156	760	100.0	156	Sequence 2, Appli
14	US-09-016-537A-2	156	760	100.0	156	Sequence 2, Appli
14	US-09-016-750-2	156	760	100.0	156	Sequence 2, Appli
14	US-09-016-750C-2	156	760	100.0	156	Sequence 2, Appli
14	US-09-016-869A-2	156	760	100.0	156	Sequence 2, Appli
23	US-09-947-206-2	156	760	100.0	156	Sequence 2, Appli
28	US-09-016-869B-2	156	760	100.0	156	Sequence 2, Appli
13	US-08-902-572-2	391	760	100.0	391	Sequence 2, Appli
18	US-09-457-568-4	391	760	100.0	391	Sequence 4, Appli
18	US-09-457-646-4	391	760	100.0	391	Sequence 4, Appli
19	US-09-516-065-4	391	760	100.0	391	Sequence 4, Appli
19	US-09-718-233-2	391	760	100.0	391	Sequence 2, Appli
6	US-08-251-938-2	148	753	99.1	148	Sequence 2, Appli
8	US-09-075-505-2	148	753	99.1	148	Sequence 2, Appli
8	US-08-474-083-2	156	753	99.1	156	Sequence 2, Appli
8	US-08-479-731-2	156	753	99.1	156	Sequence 2, Appli
8	US-08-481-063-2	156	753	99.1	156	Sequence 2, Appli
9	US-08-502-881-2	156	753	99.1	156	Sequence 2, Appli
14	US-09-021-752-2	156	753	99.1	156	Sequence 2, Appli
14	US-09-075-505-3	156	753	99.1	156	Sequence 3, Appli
16	US-09-272-233-2	156	753	99.1	156	Sequence 2, Appli
18	US-09-457-568-28	156	753	99.1	156	Sequence 28, Appli
18	US-09-457-646-28	156	753	99.1	156	Sequence 28, Appli
19	US-09-516-065-28	156	753	99.1	156	Sequence 28, Appli
20	US-09-614-099-19	156	753	99.1	156	Sequence 19, Appli
26	US-09-849-626-1908	156	753	99.1	156	Sequence 1908, Ap
26	US-10-017-754-1908	156	753	99.1	156	Sequence 1908, Ap

ALIGNMENTS

RESULT 1  
PCT-US95-03316-2  
Sequence 2, Application PC/TUS9503316  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS GENE, SOMATIC MUTATIONS IN THE MTS  
TITLE OF INVENTION: GENE, AND METHODS FOR DIAGNOSIS, PROGNOSIS AND THERAPY OF  
TITLE OF INVENTION: CANCER DUE TO THE MTS GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESS: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE:



Query Match 100.0%; Score 760; DB 6; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.4e-75;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
FILING DATE: 18-MAR-1994  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 148 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-214-581-2

Query Match 100.0%; Score 760; DB 6; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.4e-75;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MEPSADWLATAAARGVEEVRALEVALPNAAPNSYGRRPQVMMGMSARVAELLLHGA 60  
QY 61 EPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120  
DB 61 EPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120  
QY 121 YLRAAGGTGRGSHARIDAAGPSDIPD 148  
DB 121 YLRAAGGTGRGSHARIDAAGPSDIPD 148

RESULT 4  
US-08-214-582-2  
Sequence 2, Application US/08214582  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: SOMATIC MUTATIONS IN THE MTS GENE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/214,582  
FILING DATE: 18-MAR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 148 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-214-582-2

Query Match 100.0%; Score 760; DB 6; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.4e-75;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEPSADWLATAAARGVEEVRALEVALPNAAPNSYGRRPQVMMGMSARVAELLLHGA 60  
DB 1 MEPSADWLATAAARGVEEVRALEVALPNAAPNSYGRRPQVMMGMSARVAELLLHGA 60  
QY 61 EPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120  
DB 61 EPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120  
QY 121 YLRAAGGTGRGSHARIDAAGPSDIPD 148  
DB 121 YLRAAGGTGRGSHARIDAAGPSDIPD 148

RESULT 5  
US-08-215-086-2  
Sequence 2, Application US/08215086  
GENERAL INFORMATION:  
APPLICANT: Cannon-Albright, Lisa A.  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/215,086  
FILING DATE: 18-MAR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 148 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-215-086-2

Query Match 100.0%; Score 760; DB 6; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.4e-75;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MEPSADWLATAAARGVEEVRALEVALPNAAPNSYGRRPQVMMGMSARVAELLLHGA 60  
QY 61 EPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120  
DB 61 EPCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120  
QY 121 YLRAAGGTGRGSHARIDAAGPSDIPD 148  
DB 121 YLRAAGGTGRGSHARIDAAGPSDIPD 148

Db 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148

## RESULT 6

US-08-215-087-2  
; Sequence 2, Application US/08215087  
; GENERAL INFORMATION:  
; APPLICANT: Skolnick, Mark H.  
; APPLICANT: Cannon-Albright, Lisa A.  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO  
; TITLE OF INVENTION: CANCER  
; TITLE OF INVENTION: AT THE MTS GENE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/215.087  
; FILING DATE: 18-MAR-1994  
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-109348  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 148 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-215-087-2

Query Match 100.0%; Score 760; DB 6; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.4e-75;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAELLLHGA 60

Db 1 MEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAELLLHGA 60

QY 61 EPCADPATLTTPVHDAAREGFLDTLVVLRHAGARLDVRDANGRLPVDLAELGHRDVAR 120

Db 61 EPCADPATLTTPVHDAAREGFLDTLVVLRHAGARLDVRDANGRLPVDLAELGHRDVAR 120

QY 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148

Db 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148

## RESULT 7

US-08-215-088-2  
; Sequence 2, Application US/08215088  
; GENERAL INFORMATION:  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND PROGNOSIS OF  
; TITLE OF INVENTION: CANCER DUE TO THE MTS GENE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti

; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/215.088  
; FILING DATE: 18-MAR-1994  
; CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-109348  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 148 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-215-088-2

Query Match 100.0%; Score 760; DB 6; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.4e-75;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAELLLHGA 60

Db 1 MEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGMSARVAELLLHGA 60

QY 61 EPCADPATLTTPVHDAAREGFLDTLVVLRHAGARLDVRDANGRLPVDLAELGHRDVAR 120

Db 61 EPCADPATLTTPVHDAAREGFLDTLVVLRHAGARLDVRDANGRLPVDLAELGHRDVAR 120

QY 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148

Db 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148

## RESULT 8

US-08-227-369-2  
; Sequence 2, Application US/08227369  
; GENERAL INFORMATION:  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: SOMATIC MUTATIONS IN THE MTS GENE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/227,369  
; FILING DATE: 14-APR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/214,582  
; FILING DATE: 18-MAR-1994

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Imnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-227-369-2

Query Match 100.0%; Score 760; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQVMMMGSAARVAELLLHGA 60
Db 1 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQVMMMGSAARVAELLLHGA 60
Qy 61 EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRDAGRLPVDLAELGHRDVAR 120
Db 61 EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRDAGRLPVDLAELGHRDVAR 120
Qy 121 YLRAAAGTGRGSHNARIDAAEGPSDIPD 148
Db 121 YLRAAAGTGRGSHNARIDAAEGPSDIPD 148

RESULT 9
US-08-227-371-2
; Sequence 2, Application US/08227371
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Protein, and Uses
; TITLE OF INVENTION: Related Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,371
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Imnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-016-869b-35.rapm

Query Match 100.0%; Score 760; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQVMMMGSAARVAELLLHGA 60
Db 1 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQVMMMGSAARVAELLLHGA 60
Qy 61 EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRDAGRLPVDLAELGHRDVAR 120
Db 61 EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDRDAGRLPVDLAELGHRDVAR 120
Qy 121 YLRAAAGTGRGSHNARIDAAEGPSDIPD 148
Db 121 YLRAAAGTGRGSHNARIDAAEGPSDIPD 148

RESULT 10
US-09-480-135-16
; Sequence 16, Application US/09480135
; GENERAL INFORMATION:
; APPLICANT: Sherr Ph.D., Charles J.
; APPLICANT: Downing M.D., James
; APPLICANT: Hirai Ph.D., Hiroshi
; APPLICANT: Okuda, Tsukasa
; TITLE OF INVENTION: Ink4c-pl8 and Ink4d-pl9, Inhibitors of
; TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX PLLC
; STREET: 1100 New York Ave., Suite 600, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/480,135
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/384,106
; FILING DATE: 06-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0500002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-480-135-16

Query Match 100.0%; Score 760; DB 18; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQVMMMGSAARVAELLLHGA 60
```





Db 61 EPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120

Qy 121 YLRAAGGTGRGSHARIDAAEGPSDIPD 148

Db 121 YLRAAGGTGRGSHARIDAAEGPSDIPD 148

## RESULT 13

US-08-248-812-2

; Sequence 2, Application US/08248812

; GENERAL INFORMATION:

; APPLICANT: Beach, David H.

; APPLICANT: Demetrick, Douglas J.

; APPLICANT: Serrano, Manuel

; APPLICANT: Hannon, Gregory J.

; APPLICANT: Queller, Dawn E.

; APPLICANT: Sherr, Charles J.

; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses

; TITLE OF INVENTION: Related Thereto

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/248,812

; FILING DATE: 25-MAY-1994

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: CSI-001CP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 156 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-248-812-2

## Query Match

Best Local Similarity 100.0%; Score 760; DB 6; Length 156;

Mismatches 0; Indels 0; Gaps 0;

Matches 148; Conservative 0;

Qy 1 MEPSADWLATAAARGVEEVRALEAVLNPNSYGRRPVQVMMGSAVALLLHGA 60

Db 9 MEPSADWLATAAARGVEEVRALEAVLNPNSYGRRPVQVMMGSAVALLLHGA 68

Qy 61 EPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120

Db 69 EPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 128

Qy 121 YLRAAGGTGRGSHARIDAAEGPSDIPD 148

Db 129 YLRAAGGTGRGSHARIDAAEGPSDIPD 156

## RESULT 14

US-08-306-511-2

; Sequence 2, Application US/08306511

; GENERAL INFORMATION:

; APPLICANT: Beach, David H.

; APPLICANT: Demetrick, Douglas J.

; APPLICANT: Serrano, Manuel

; APPLICANT: Hannon, Gregory J.

; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses

; TITLE OF INVENTION: Related Thereto

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/306,511

; FILING DATE: 14-SEP-1994

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: CSI-001CP2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 156 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-306-511-2

## Query Match

Best Local Similarity 100.0%; Score 760; DB 7; Length 156;

Mismatches 0; Indels 0; Gaps 0;

Matches 148; Conservative 0;

Qy 1 MEPSADWLATAAARGVEEVRALEAVLNPNSYGRRPVQVMMGSAVALLLHGA 60

Db 9 MEPSADWLATAAARGVEEVRALEAVLNPNSYGRRPVQVMMGSAVALLLHGA 68

Qy 61 EPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 120

Db 69 EPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAELGHRDVAR 128

Qy 121 YLRAAGGTGRGSHARIDAAEGPSDIPD 148

Db 129 YLRAAGGTGRGSHARIDAAEGPSDIPD 156

## RESULT 15

US-08-497-214A-2

; Sequence 2, Application US/08497214A

; GENERAL INFORMATION:

; APPLICANT: Beach, David H.

; APPLICANT: Demetrick, Douglas J.

; APPLICANT: Serrano, Manuel

; APPLICANT: Hannon, Gregory

; TITLE OF INVENTION: Cell-cycle Regulatory Proteins and

; TITLE OF INVENTION: Uses Related Thereto

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley, Hoag & Eliot LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/497,214A  
FILING DATE: 30-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV071.05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1000  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-497-214A-2

Query Match 100.0%; Score 760; DB 8; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.5e-75;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEPSADWLATAAARGVEVRALLEVALPNAPNSYGRRPQVMMMGSAARVAELLLHGA 60  
DB 9 MEPSADWLATAAARGVEVRALLEVALPNAPNSYGRRPQVMMMGSAARVAELLLHGA 68  
QY 61 EPCNADPATLTRPVHDAAREGEFDTLVVLHAGARLDVRDANGRLPVDLAELGHRDVAR 120  
DB 69 EPCNADPATLTRPVHDAAREGEFDTLVVLHAGARLDVRDANGRLPVDLAELGHRDVAR 128  
QY 121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148  
DB 129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156

Search completed: May 7, 2002, 12:35:37  
Job time: 207 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:32:40 ; Search time 8.7 seconds  
(without alignments)  
239.553 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 760

Sequence: 1 MEPSADWLATAAARGVEEV.....TRGSNHARIDAEGSPDIPD 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 64870 seqs, 14081815 residues

Total number of hits satisfying chosen parameters: 64870

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA\_New:\*

- 1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/paa/US05\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	753	99.1	156	1	PCT-US02-07826-41
2	753	99.1	156	5	US-09-947-206D-2
3	753	99.1	156	5	US-09-947-206C-2
4	753	99.1	156	6	US-10-097-340-41
5	753	99.1	156	6	US-10-113-872-1908
6	627.5	82.6	157	5	US-09-947-206D-12
7	627.5	82.6	157	5	US-09-947-206C-12
8	493.5	64.9	137	5	US-09-947-206D-4
9	493.5	64.9	137	5	US-09-947-206C-4
10	382	50.3	138	5	US-09-947-206D-13
11	382	50.3	138	5	US-09-947-206C-13
12	356	46.8	77	5	US-09-947-206D-8
13	356	46.8	77	5	US-09-947-206C-8
14	330	43.4	125	5	US-09-947-206D-6
15	330	43.4	125	5	US-09-947-206C-6
16	299.5	39.4	85	5	US-09-947-206D-11
17	299.5	39.4	85	5	US-09-947-206C-11
18	299.5	39.4	127	5	US-09-947-206D-14
19	299.5	39.4	127	5	US-09-947-206C-14
20	228.5	30.1	168	6	US-10-113-872-1907
21	149.5	19.7	1360	1	PCT-US02-09288-12
22	146	19.2	1166	5	US-09-972-115A-6
23	137	18.0	1327	5	US-09-972-115A-8
24	136	17.9	399	1	PCT-US02-09288-23
25	131	17.2	844	5	US-09-573-655B-1268
26	129	17.0	1536	1	PCT-US02-09944-470

RESULT 1  
PCT-US02-07826-41  
; Sequence 41, Application PC/TUS0207826  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
; FILE REFERENCE: Assessment, Prevention, and Therapy of Ovarian Cancer  
; CURRENT APPLICATION NUMBER: PCT/US02/07826  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 60/276,025  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/325,149  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: 60/276,026  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/324,967  
; PRIOR FILING DATE: 2001/09/26  
; PRIOR APPLICATION NUMBER: 60/311,732  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/325,102  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/323,580  
; PRIOR FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 363  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 41  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-07826-41

#### ALIGNMENTS

27	126	16.6	1333	5	US-09-972-115A-2	Sequence 2, Appli
28	124.5	16.4	349	1	PCT-US02-09944-451	Sequence 451, App
29	124.5	16.4	608	1	PCT-US02-09944-708	Sequence 708, App
30	122	16.1	182	1	PCT-US02-09944-429	Sequence 429, App
31	121	15.9	877	5	US-09-573-655B-941	Sequence 941, App
32	113.5	14.9	1715	6	US-10-117-229-6	Sequence 6, Appli
33	112.5	14.8	1715	1	PCT-US02-09288-26	Sequence 26, Appli
34	112.5	14.8	1715	6	US-10-117-229-2	Sequence 2, Appli
35	112	14.7	556	1	PCT-US02-09944-427	Sequence 427, App
36	111.5	14.7	1267	5	US-09-972-115A-4	Sequence 4, Appli
37	110	14.5	1270	1	PCT-US02-09944-696	Sequence 696, App
38	110	14.5	2067	1	PCT-US02-09944-778	Sequence 778, App
39	109.5	14.4	305	7	US-60-365-384-514	Sequence 514, App
40	109.5	14.4	305	7	US-60-365-384-515	Sequence 515, App
41	109.5	14.4	784	7	US-60-371-507-2	Sequence 2, Appli
42	109.5	14.4	1060	1	PCT-US02-09944-452	Sequence 452, App
43	108	14.2	654	6	US-10-002-945-123	Sequence 123, App
44	108	14.2	1762	6	US-10-117-229-7	Sequence 7, Appli
45	107	14.1	669	6	US-10-002-945-40	Sequence 40, Appli

Query Match 99.1%; Score 753; DB 1; Length 156;  
Best Local Similarity 99.3%; Pred. No. 1.le-69;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MEPSADWLATAAARGVEEVRLLEVALPAPNSYGRPIQVMMGSAVLAELLHGA 60  
Db 9 MEPSADWLATAAARGVEEVRLLEVALPAPNSYGRPIQVMMGSAVLAELLHGA 68  
Qy 61 EPNCADPATLTPRVHDAAREGFLDTLVLRHAGARLDVRDANGRLPVDLAELGHRDVAR 120  
Db 69 EPNCADPATLTPRVHDAAREGFLDTLVLRHAGARLDVRDANGRLPVDLAELGHRDVAR 128  
Qy 121 YLRAAAGTGRGSHARIDAEGSPDIPD 148  
Db 129 YLRAAAGTGRGSHARIDAEGSPDIPD 156













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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:30:35 ; Search time 12.51 seconds  
(without alignments)  
266.226 Million cell updates/sec

Title: US-09-016-869B-35

Perfect score: 760

Sequence: 1 MEPSADWLATAAARGVEEV.....TRGSNHRIDAAGPSDIPD 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued\_Patents\_AA.\*

1: /cgn2.6/ptodata/2/iaa/5A\_COMB.pep.\*

2: /cgn2.6/ptodata/2/iaa/5B\_COMB.pep.\*

3: /cgn2.6/ptodata/2/iaa/6A\_COMB.pep.\*

4: /cgn2.6/ptodata/2/iaa/6B\_COMB.pep.\*

5: /cgn2.6/ptodata/2/iaa/PCTUS\_COMB.pep.\*

6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	760	100.0	148	1 US-08-154-915-4	Sequence 4, Appli
2	760	100.0	148	3 US-08-384-106A-16	Sequence 16, Appl
3	760	100.0	148	3 US-08-384-106A-24	Sequence 24, Appl
4	760	100.0	148	5 PCT-US93-09945-4	Sequence 4, Appli
5	760	100.0	156	2 US-08-627-610-2	Sequence 2, Appli
6	760	100.0	156	2 US-08-306-511A-2	Sequence 2, Appli
7	760	100.0	156	2 US-08-893-274-2	Sequence 2, Appli
8	760	100.0	156	3 US-08-581-918A-2	Sequence 2, Appli
9	760	100.0	156	4 US-08-346-147B-2	Sequence 2, Appli
10	760	100.0	156	4 US-08-822-936-2	Sequence 2, Appli
11	760	100.0	156	5 PCT-US95-04636-2	Sequence 2, Appli
12	760	100.0	391	1 US-08-589-981-2	Sequence 2, Appli
13	753	99.1	156	1 US-08-474-177-2	Sequence 2, Appli
14	753	99.1	156	1 US-08-487-033-2	Sequence 2, Appli
15	753	99.1	156	1 US-08-480-810-2	Sequence 2, Appli
16	753	99.1	156	2 US-08-508-735-2	Sequence 2, Appli
17	753	99.1	156	2 US-08-848-251-2	Sequence 2, Appli
18	753	99.1	156	2 US-08-486-047-2	Sequence 2, Appli
19	753	99.1	156	3 US-09-120-130-2	Sequence 2, Appli
20	753	99.1	156	3 US-09-115-252-2	Sequence 2, Appli
21	753	99.1	156	3 US-08-986-515-2	Sequence 2, Appli
22	753	99.1	156	4 US-09-120-128-2	Sequence 2, Appli
23	753	99.1	156	4 US-09-120-129-2	Sequence 2, Appli
24	753	99.1	156	4 US-09-201-139-2	Sequence 2, Appli
25	753	99.1	156	4 US-09-120-131-2	Sequence 2, Appli
26	753	99.1	156	4 US-08-910-722-2	Sequence 2, Appli
27	749.5	98.6	157	5 PCT-US96-05252-5	Sequence 5, Appli

28 627.5 82.6 157 3 US-08-581-918A-12 Sequence 12, Appli  
29 627.5 82.6 157 4 US-08-346-147B-12 Sequence 12, Appli  
30 544 71.6 105 1 US-08-474-177-14 Sequence 14, Appli  
31 544 71.6 105 1 US-08-487-033-14 Sequence 14, Appli  
32 544 71.6 105 1 US-08-480-810-14 Sequence 14, Appli  
33 544 71.6 105 2 US-08-508-735-14 Sequence 14, Appli  
34 544 71.6 105 2 US-08-848-251-14 Sequence 14, Appli  
35 544 71.6 105 2 US-08-486-047-14 Sequence 14, Appli  
36 544 71.6 105 3 US-09-120-130-14 Sequence 14, Appli  
37 544 71.6 105 3 US-09-115-252-14 Sequence 14, Appli  
38 544 71.6 105 3 US-08-986-515-14 Sequence 14, Appli  
39 544 71.6 105 4 US-09-120-128-14 Sequence 14, Appli  
40 544 71.6 105 4 US-09-120-129-14 Sequence 14, Appli  
41 544 71.6 105 4 US-09-201-139-14 Sequence 14, Appli  
42 544 71.6 105 4 US-09-120-131-14 Sequence 14, Appli  
43 533 70.1 130 2 US-08-627-610-8 Sequence 8, Appli  
44 533 70.1 130 3 US-08-581-918A-8 Sequence 8, Appli  
45 533 70.1 130 4 US-08-346-147B-8 Sequence 8, Appli

#### ALIGNMENTS

RESULT 1  
US-08-154-915-4  
; Sequence 4, Application US/08154915  
; Patent No. 5618669  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David  
; APPLICANT: Xiong, Yue  
; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses  
; TITLE OF INVENTION: Related Thereto  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/154,915  
; FILING DATE: 19-NOV-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/991,997  
; FILING DATE: 17-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/963,308  
; FILING DATE: 16-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/888,178  
; FILING DATE: 26-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/701,514  
; FILING DATE: 16-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: MII-026  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 148 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-08-154-915-4

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Query Match          100.0%; Score 760; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

QY 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148  
+ + + + +  
Db 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148

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RESULT      2
US-08-384-106A-16
; Sequence 16, Application US/08384106A
; Patent No. 6033847
;
; GENERAL INFORMATION:
;
; APPLICANT: Sherr Ph.D., Charles J.
; APPLICANT: Downing M.D., James
; APPLICANT: Hirai Ph.D., Hiroshi
; APPLICANT: Okuda, Tsukasa
;
; TITLE OF INVENTION: InK4c-p18 and InK4d-p19, Inhibitors of
; TITLE OF INVENTION: Cyclin dependent Kinases CDK4 and CDK6, and Uses Thereof
;
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
;

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Query Match	100.0%;	Score 760;	DB 3;	Length 148;
Best Local Similarity	100.0%;	Pred. No. 1.5e-83;		
Matches 148:	Conservative	0;	Mismatches 0;	Indels 0;
	Gaps	0;		

**QY**

1 MEPSADWLATAAARGRVEEVRALEAVLPNAPNSYGRRPIQVMMGSA RVAELLHGA 60  
|||||

**db**

1 MEPSADWLATAAARGRVEEVRALEAVLPNAPNSYGRRPIQVMMGSA RVAELLHGA 60  
|||||

Qy	61	EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDAWGRLPYDLAEELGCHRDVAR	120
Db	61	EPNCADPATLTPRVHDAAREGFLDTLVVLRAGARLDVDAWGRLPYDLAEELGHRDVAR	120
Qy	121	YLRAAAGGTGRGNSNHARIDAAEGPSDIPD	148
Db	121	YLRAAAGGTGRGNSNHARIDAAEGPSDIPD	148

RESULT 3  
US-08-384-106A-24  
; Sequence 24, Application US/08384106A  
; Patent No. 6033847  
; GENERAL INFORMATION:  
; APPLICANT: Sherr Ph.D., Charles J.  
; APPLICANT: Downing M.D., James  
; APPLICANT: Hirai Ph.D., Hiroshi  
; APPLICANT: Okuda, Tsukasa  
; TITLE OF INVENTION: InK4c-p18 and InK4d-p19, Inhibitors of  
; TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005

Query Match 100.0%; Score 760; DB 3; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.5e-83;  
Matches 148. Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPSADWLATAAARGVEEVRALLEAVLPNAPNSYGRRP	IOVMNMGSRVAEALLLHGA	60
Db	1	MEPSADWLATAAARGVEEVRALLEAVLPNAPNSYGRRP	IOVMNMGSRVAEALLLHGA	60
Qy	61	EPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDV	RDAMGRLPVDLAEELGHRDVAR	120
Db	61	EPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDV	RDAMGRLPVDLAEELGHRDVAR	120
Qy	121	YLRAAAGGTRGNSNHARIDAAREGSPDIPD	148	
Db	121	YLRAAAGGTRGNSNHARIDAAREGSPDIPD	148	

## RESULT

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PCT-US93-09945-4
; Sequence 4, Application PC/TUS9309945
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses Related
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09945
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-09945-4

Query Match 100.0%; Score 760; DB 5; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.5e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPVQVMMGMSARVAELLLHGA 60
Db 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPVQVMMGMSARVAELLLHGA 60

QY 61 EPNCADPATLTTPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
Db 61 EPNCADPATLTTPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120

QY 121 YLRAAGGTGSGNHARIDAEGPSDIPD 148
Db 121 YLRAAGGTGSGNHARIDAEGPSDIPD 148

RESULT 5
US-08-627-610-2
; Sequence 2, Application US/08627610
; Patent No. 591997
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Serrano, Manuel
; APPLICANT: Depinho, Ronald A.
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,610
; FILING DATE: 04-APR-1996
```

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; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-627-610-2

Query Match 100.0%; Score 760; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPVQVMMGMSARVAELLLHGA 60
Db 9 MEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPVQVMMGMSARVAELLLHGA 68

QY 61 EPNCADPATLTTPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 120
Db 69 EPNCADPATLTTPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEEELGHRDVAR 128

QY 121 YLRAAGGTGSGNHARIDAEGPSDIPD 148
Db 129 YLRAAGGTGSGNHARIDAEGPSDIPD 156

RESULT 6
US-08-306-511A-2
; Sequence 2, Application US/08306511A
; Patent No. 5962316
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,511A
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/991,997  
;; FILING DATE: 17-DEC-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Vincent, Matthew P.  
;; REGISTRATION NUMBER: 36,709  
;; REFERENCE/DOCKET NUMBER: MIV-071.06  
;; TELEPHONE: (617) 832-1299  
;; TELEFAX: (617) 832-7000  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 156 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-581-918A-2

Query Match 100.0%; Score 760; DB 3; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.6e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSAARVAELLHLHGA 60  
Db 9 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSAARVAELLHLHGA 68  
QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 120  
Db 69 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 128  
QY 121 YLRAAAGTGRGSHARIDAAEGPSDIPD 148  
Db 129 YLRAAAGTGRGSHARIDAAEGPSDIPD 156

RESULT 9  
US-08-346-147B-2  
;; Sequence 2, Application US/08346147B  
;; Patent No. 6211334  
;; GENERAL INFORMATION:  
;; APPLICANT: Beach, David H.  
;; APPLICANT: Demetrick, Douglas J.  
;; APPLICANT: Serrano, Manuel  
;; APPLICANT: Hannon, Gregory J.  
;; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
;; TITLE OF INVENTION: Related Thereto  
;; NUMBER OF SEQUENCES: 47  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Foley, Hoag & Eliot  
;; STREET: One Post Office Square  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02109  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: WordPad  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/346,147B  
;; FILING DATE: 29-NOV-1994  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/306,511  
;; FILING DATE: 14-SEP-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/248,812  
;; FILING DATE: 25-MAY-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/227,371  
;; FILING DATE: 14-APR-1994

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/154,915  
;; FILING DATE: 18-NOV-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/991,997  
;; FILING DATE: 17-DEC-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Vincent, Matthew P.  
;; REGISTRATION NUMBER: 36,709  
;; REFERENCE/DOCKET NUMBER: MIV-071.04  
;; TELEPHONE: (617) 832-1299  
;; TELEFAX: (617) 832-7000  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 156 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-346-147B-2

Query Match 100.0%; Score 760; DB 4; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.6e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSAARVAELLHLHGA 60  
Db 9 MEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSAARVAELLHLHGA 68  
QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 120  
Db 69 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 128  
QY 121 YLRAAAGTGRGSHARIDAAEGPSDIPD 148  
Db 129 YLRAAAGTGRGSHARIDAAEGPSDIPD 156

RESULT 10  
US-08-822-936-2  
;; Sequence 2, Application US/08822936  
;; Patent No. 6242575  
;; GENERAL INFORMATION:  
;; APPLICANT: Massague, Joan  
;; APPLICANT: Roberts, James M.  
;; APPLICANT: Koff, Andrew  
;; APPLICANT: Polyak, Kornelia  
;; TITLE OF INVENTION: Isolated P27 Protein, Nucleic Acid  
;; TITLE OF INVENTION: Molecules Encoding Same, Methods of Identifying Agents Acti  
;; TITLE OF INVENTION: and Uses of Said Agents  
;; NUMBER OF SEQUENCES: 10  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Foley, Hoag & Eliot, LLP  
;; STREET: One Post Office Square  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02109-2170  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/822,936  
;; FILING DATE: 21-FEBRUARY-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Vincent, Matthew P.  
;; REGISTRATION NUMBER: 36,709  
;; REFERENCE/DOCKET NUMBER: MIV-079.05  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 832-1000

RESULT 13  
US-08-474-177-2  
; Sequence 2, Application US/08474177  
; Patent No. 5624819

GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,177  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-177-2

Query Match 99.1%; Score 753; DB 1; Length 156;  
Best Local Similarity 99.3%; Pred. No. 1.1e-82;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MPEPSADWLATAARGVEEVRLLEAVLPNAPNSYGRPRPIQVMMGMSARVAELLLHGA 60  
|||||  
DB 9 MPEPSADWLATAARGVEEVRLLEAGALPNAPNSYGRPRPIQVMMGMSARVAELLLHGA 68  
QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 120  
DB 69 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 128  
QY 121 YLRAAAGGTRGSNHARIDAEGPSDIPD 148  
DB 129 YLRAAAGGTRGSNHARIDAEGPSDIPD 156

RESULT 14  
US-08-487-033-2  
Sequence 2, Application US/08487033  
Patent No. 5739027  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1E1-Beta GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,033  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-487-033-2

Query Match 99.1%; Score 753; DB 1; Length 156;  
Best Local Similarity 99.3%; Pred. No. 1.1e-82;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MPEPSADWLATAARGVEEVRLLEAVLPNAPNSYGRPRPIQVMMGMSARVAELLLHGA 60  
|||||  
DB 9 MPEPSADWLATAARGVEEVRLLEAGALPNAPNSYGRPRPIQVMMGMSARVAELLLHGA 68  
QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 120  
DB 69 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDANGRLPVDLAEEELGHRDVAR 128  
QY 121 YLRAAAGGTRGSNHARIDAEGPSDIPD 148  
DB 129 YLRAAAGGTRGSNHARIDAEGPSDIPD 156

RESULT 15  
US-08-480-810-2  
; Sequence 2, Application US/08480810  
; Patent No. 5801236  
; GENERAL INFORMATION:  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: MTS1 GENE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,810  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/03316  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/251,938  
; FILING DATE: 01-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,087  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,086  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,369  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/214,582  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-109348  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 156 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-480-810-2

Query Match 99.1%; Score 753; DB 1; Length 156;  
Best Local Similarity 99.3%; Pred. No. 1.le-82;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MEPSADWLATAAARGVEEVRALLEAVLPNAPNSYGRRPPIQVMMGMSARVAELLHGA 60  
Db 9 MEPSADWLATAAARGVEEVRALLEAGALPNAPNSYGRRPPIQVMMGMSARVAELLHGA 68  
Qy 61 EPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAEELGHRDVAR 120  
Db 69 EPNCADPATLTPRVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAEELGHRDVAR 128  
Qy 121 YLRAAAGTGRGSHARIDAAEGPSDIPD 148

Db 129 YLRAAAGTGRGSHARIDAAEGPSDIPD 156  
Search completed: May 7, 2002, 12:33:23  
Job time: 168 sec